

Refine Search

Search Results -

Term	Documents
(3 NOT 4).PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD.	3
(L3 NOT L4).PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD.	3

Database:

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 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L5

Search History

DATE: Wednesday, November 15, 2006

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Set Name Query
 side by side

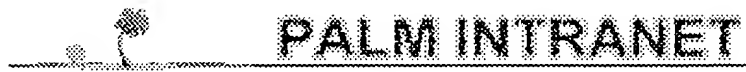
Hit Count

Set
Name
 result set

DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; THES=ASSIGNEE; PLUR=YES;
 OP=AND

<u>L5</u>	L3 not L4	3	<u>L5</u>
<u>L4</u>	L3 and (oedema or diarrhia)	7	<u>L4</u>
<u>L3</u>	(porcine or swine) same (FUT1 and polymorphism)	10	<u>L3</u>
<u>L2</u>	Bosworth-Brad-T\$.in.	8	<u>L2</u>
<u>L1</u>	Bosworth-Brad.in.	1	<u>L1</u>

END OF SEARCH HISTORY



Day : Wednesday

Date: 11/15/2006

Time: 16:38:50

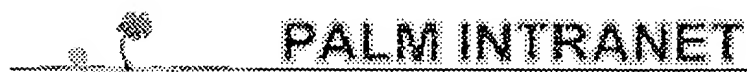
Inventor Name Search

Enter the **first few letters** of the Inventor's Last Name.
Additionally, enter the **first few letters** of the Inventor's First name.

Last Name**First Name**

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Day : Wednesday

Date: 11/15/2006

Time: 16:38:50

Inventor Name Search

Enter the first few letters of the Inventor's Last Name.
Additionally, enter the first few letters of the Inventor's First name.

Last Name**First Name**

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SCORE Search Results Details for Application 09844268 and Search Result us-09-844-268-12.rge.

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OM nucleic - nucleic search, using sw model

Run on: November 13, 2006, 16:38:38 ; Search time 7441 Seconds
(without alignments)
10905.695 Million cell updates/sec

Title: US-09-844-268-12
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

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- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1269	100.0	1269	2	AR360893	AR360893 Sequence
3	1269	100.0	1269	2	AR771735	AR771735 Sequence
4	1269	100.0	1269	2	AX752829	AX752829 Sequence
5	1264.2	99.6	1269	2	AR200399	AR200399 Sequence
6	1261	99.4	1269	14	PIGFTF	I50534 Pig (Sus sc
7	1245.8	98.2	3315	14	U70883	U70883 Sus scrofa
8	1245	98.1	2528	14	AF136896	AF136896 Sus scrof
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ALIGNMENTS

RESULT 1
BD085288

LOCUS BD085288 1269 bp DNA linear PAT 27-AUG-2002
 DEFINITION Methods and compositions to identify swine genetically resistant to F18 E coli associated diseases.
 ACCESSION BD085288
 VERSION BD085288.1 GI:22630898
 KEYWORDS JP 2001521401-A/12.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.
 REFERENCE 1 (bases 1 to 1269)
 AUTHORS Bosworth,B.T. and Vogeli,P.
 TITLE Methods and compositions to identify swine genetically resistant to F18 E coli associated diseases
 JOURNAL Patent: JP 2001521401-A 12 06-NOV-2001;
 BIOTECHNOLOGY RESEARCH AND DEVELOPMENT CORP, US DEPARTMENT OF AGRICULTURE, SWISS FEDERAL INSTITUTE OF TECHNOLOGY ZURICH
 COMMENT OS Unidentified
 PN JP 2001521401-A/12
 PD 06-NOV-2001
 PF 20-MAY-1998 JP 1998550579
 PR 20-MAY-1997 US 60/047181
 PI BRAD T BOSWORTH,PETER VOGELI
 PC C12Q1/68,C07K14/47
 CC Strandedness: Single;
 CC Topology: Linear;
 CC Methods and compositions to identify swine genetically resistant to F18 E coli associated diseases
 FH Key Location/Qualifiers
 FT CDS 9..1103.
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
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RESULT 2

AR360893

LOCUS AR360893 1269 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 12 from patent US 6596923.

ACCESSION AR360893

VERSION AR360893.1 GI:33768402

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1269)

AUTHORS Bosworth, B.T. and Vogeli, P.

TITLE Methods and compositions to identify swine genetically resistant to F18 E. coli associated diseases

JOURNAL Patent: US 6596923-A 12 22-JUL-2003;
Biotechnology Research & Development Corp., The United States of America as represented by the Secretary of Agriculture and Swiss Federal Institute of Technology; Peoria, IL

FEATURES Location/Qualifiers

source 1. 1269

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1269; DB 2; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	421		ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Qy	481		AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	481		AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
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Db	541		GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Qy	601		TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCGAGCACCTTCGTGGGGGTCC	660
Db	601		TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCGAGCACCTTCGTGGGGGTCC	660
Qy	661		ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
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AR771735

LOCUS AR771735 1269 bp DNA linear PAT 08-DEC-2005

DEFINITION Sequence 12 from patent US 6965022.

ACCESSION AR771735

VERSION AR771735.1 GI:83347396

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1269)

AUTHORS Bosworth, B.T. and Vogeli, P.

TITLE Methods to identify swine genetically resistant to F18 E. coli associated diseases

JOURNAL Patent: US 6965022-A 12 15-NOV-2005;
The United States of America as represented by the Secretary of
Agriculture and Swiss Federal Institute of Technology; Washington,
DC

FEATURES

source

Location/Qualifiers

1. .1269

/organism="unknown"

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ORIGIN

Query Match 100.0%; Score 1269; DB 2; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	901	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
QY	961	CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
Db	961	CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
QY	1021	TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGCTCTC	1080
Db	1021	TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGCTCTC	1080
QY	1081	CACTCCAGATGTTGGCTGGGCCCTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Db	1081	CACTCCAGATGTTGGCTGGGCCCTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
QY	1141	AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAAGTTCGGAGATGCTGGTGG	1200
Db	1141	AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAAGTTCGGAGATGCTGGTGG	1200
QY	1201	TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Db	1201	TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
QY	1261	ACCCTGCAG	1269
Db	1261	ACCCTGCAG	1269

RESULT 4
AX752829

LOCUS AX752829 1269 bp mRNA linear PAT 20-JUN-2003
 DEFINITION Sequence 12 from Patent EP1310570.
 ACCESSION AX752829
 VERSION AX752829.1 GI:32134722
 KEYWORDS .
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 REFERENCE 1
 AUTHORS Bosworth,B.T. and Voegeli,P.
 TITLE Methods and compositions to identify swine genetically resistant to
 F18 E. coli associated diseases
 JOURNAL Patent: EP 1310570-A 12 14-MAY-2003;
 Biotechnology Research and Development Corporation (US); U.S.
 Department Of Agriculture (US) ; Swiss Federal Institute of
 Technology Zurich (CH)
 FEATURES Location/Qualifiers
 source 1. .1269
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 gene 1. .1269
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 CDS 9. .1106
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 /product="alpha (1,2) fucosyltransferase"
 /protein_id="CAD99177.1"
 /db_xref="GI:32134723"
 /translation="MWVPSRRHLCITFLLVCVLAAIFFLNQYQDLFYSGLDLLALCPD
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ORIGIN

Query Match 100.0%; Score 1269; DB 2; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
QY	61	TTTGTAGCAGCAATTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
Db	61	TTTGTAGCAGCAATTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
QY	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Db	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
QY	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCCGTGTCCTCAAGCATCTGCCTCCTTTT	240
Db	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCCGTGTCCTCAAGCATCTGCCTCCTTTT	240
QY	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACAGATGGGACAGTATGCCA	300

Db	241		CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
QY	301		CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
Db	301		CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
QY	361		CCGTCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCCGAGGTAGACAGGC	420
Db	361		CCGTCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCCGAGGTAGACAGGC	420
QY	421		ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCCACTTAA	480
Db	421		ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCCACTTAA	480
QY	481		AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	481		AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
QY	541		GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
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QY	601		TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	601		TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
QY	661		ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	661		ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
QY	721		ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
Db	721		ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
QY	781		TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	781		TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
QY	841		ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
Db	841		ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
QY	901		TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
Db	901		TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
QY	961		CTGGTGGAGATACCATCTACTTGGCTAACTTACCCTGCCCCTTCCAGCTTCTTGAAGA	1020
Db	961		CTGGTGGAGATACCATCTACTTGGCTAACTTACCCTGCCCCTTCCAGCTTCTTGAAGA	1020
QY	1021		TCTTTAAACCCGAGGCTGCCTTCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Db	1021		TCTTTAAACCCGAGGCTGCCTTCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
QY	1081		CACTCCAGATGTTGGCTGGGCCCTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Db	1081		CACTCCAGATGTTGGCTGGGCCCTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
QY	1141		AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG	1200

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Db      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTCCGGAGATGCTGGTGG 1200
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Db      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
QY      1261 ACCCTGCAG 1269
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Db      1261 ACCCTGCAG 1269
    
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RESULT 5

AR200399

LOCUS AR200399 1269 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 1 from patent US 6355859.

ACCESSION AR200399

VERSION AR200399.1 GI:20250473

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1269)

AUTHORS Bosworth, B., Ridpath, J. and Wiseman, B.

TITLE Interactions between genotype and diet in swine that prevent E. coli associated intestinal disease

JOURNAL Patent: US 6355859-A 1 12-MAR-2002;

FEATURES

source

Location/Qualifiers

1. .1269

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 99.6%; Score 1264.2; DB 2; Length 1269;
 Best Local Similarity 99.8%; Pred. No. 9.4e-313;
 Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      61 TTTTAGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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Db      61 TTTTAGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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QY      181 CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT 240
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Db      181 CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT 240
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Db      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACG 360
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Db	421		ACGCTCCTTGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Qy	481		AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	481		AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Qy	541		GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Db	541		GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Qy	601		TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	601		TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Qy	661		ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	661		ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Qy	721		ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCGTCT	780
Db	721		ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCGTCT	780
Qy	781		TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	781		TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Qy	841		ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
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Qy	901		TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
Db	901		TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
Qy	961		CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
Db	961		CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
Qy	1021		TCTTTAAACCCGAGGCTGCCTTCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGCTCTC	1080
Db	1021		TCTTTAAACCCGAGGCTGCCTTCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGCTCTC	1080
Qy	1081		CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Db	1081		CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Qy	1141		AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG	1200
Db	1141		AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG	1200
Qy	1201		TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Db	1201		TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Qy	1261		ACCCTGCAG	1269

Db 1261 ACCCTGCAG 1269

RESULT 6

PIGTF

LOCUS PIGTF 1269 bp DNA linear MAM 27-JUN-1996

DEFINITION Pig (Sus scrofa) alpha,2 fucosyltransferase gene, complete cds.

ACCESSION L50534

VERSION L50534.1 GI:1395136

KEYWORDS fucosyltransferase; glycosyltransferase.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 1269)

AUTHORS Cohny,S., Mouhtouris,E., McKenzie,I.F. and Sandrin,M.S.

TITLE Molecular cloning of the gene coding for pig alpha1-->2fucosyltransferase

JOURNAL Immunogenetics 44 (1), 76-79 (1996)

PUBMED 8613146

COMMENT Original source text: Sus scrofa (tissue library: genomic) DNA.

FEATURES Location/Qualifiers

source 1. .1269

/organism="Sus scrofa"

/mol_type="genomic DNA"

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5'UTR 1. .8

CDS 9. .1106

/codon_start=1

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/db_xref="GI:1395137"

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3'UTR 1107. .1269

ORIGIN

Query Match 99.4%; Score 1261; DB 14; Length 1269;

Best Local Similarity 99.6%; Pred. No. 5.7e-312;

Matches 1264; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db	181	CGGGCACGCCGGTACACCCCAACGCCTCCGATTCTGTGCCAAGCATCCTGCCTCCTTTT	240
Qy	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Db	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Qy	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACG	360
Db	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACG	360
Qy	361	CCGTCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
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Qy	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Db	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Qy	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
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Qy	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCGAGCACCTTCGTGGGGGTCC	660
Db	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCGAGCACCTTCGTGGGGGTCC	660
Qy	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
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Qy	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Qy	841	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
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Db	901	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCTACCTGG	960
Qy	961	CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
Db	961	CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
Qy	1021	TCTTTAAACCCGAGGCTGCCTTCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Db	1021	TCTTTAAACCCGAGGCTGCCTTCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
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QY      1201  TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
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Db      1201  TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
QY      1261  ACCCTGCAG 1269
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Db      1261  ACCCTGCAG 1269

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RESULT 7

U70883

LOCUS U70883 3315 bp DNA linear MAM 12-OCT-2005

DEFINITION Sus scrofa alpha(1,2)fucosyltransferase (FUT1) gene, complete cds.

ACCESSION U70883

VERSION U70883.2 GI:4680729

KEYWORDS .

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 337 to 1844)

AUTHORS Meijerink,E., Fries,R., Vogeli,P., Masabanda,J., Wigger,G., Stricker,C., Neuenschwander,S., Bertschinger,H.U. and Stranzinger,G.

TITLE Two alpha(1,2) fucosyltransferase genes on porcine chromosome 6q11 are closely linked to the blood group inhibitor (S) and Escherichia coli F18 receptor (ECF18R) loci

JOURNAL Mamm. Genome 8 (10), 736-741 (1997)

PUBMED 9321466

REFERENCE 2 (bases 337 to 1844)

AUTHORS Meijerink,E., Fries,R., Voegeli,P. and Stranzinger,G.

TITLE Direct Submission

JOURNAL Submitted (17-SEP-1996) Animal Science, Swiss Federal Institute of Technology, Tannenstrasse 1, Zurich, ZH CH-8092, Switzerland

REFERENCE 3 (bases 1 to 3315)

AUTHORS Meijerink,E., Fries,R., Voegeli,P. and Stranzinger,G.

TITLE Direct Submission

JOURNAL Submitted (26-APR-1999) Animal Science, Swiss Federal Institute of Technology, Tannenstrasse 1, Zurich, ZH CH-8092, Switzerland

REMARK Sequence update by submitter

COMMENT On Apr 26, 1999 this sequence version replaced gi:2558692.

FEATURES

Location/Qualifiers

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gene <1. .3046
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5'UTR      join(<1. .50,607. .608)
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ORIGIN

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Query Match      98.2%; Score 1245.8; DB 14; Length 3315;
Best Local Similarity 99.4%; Pred. No. 3.8e-308;
Matches 1261; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY      1 CTGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
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Db      601 CTGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 660

QY      61 TTTTAGCAGCAATTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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Db      661 TTTTAGCAGCAATTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 720

QY      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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Db      721 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 780

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Qy	181	CGGGCACGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT	240
Db	781	CGGGCACGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT	840
Qy	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Db	841	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	900
Qy	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
Db	901	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	960
Qy	361	CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
Db	961	CCGTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	1020
Qy	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Db	1021	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	1080
Qy	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	1081	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	1140
Qy	541	GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Db	1141	GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	1200
Qy	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	1201	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	1260
Qy	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	1261	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	1320
Qy	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
Db	1321	ATGGCGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	1380
Qy	781	TTGTGGTCAACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	1381	TTGTGGTCAACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	1440
Qy	841	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
Db	1441	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	1500
Qy	901	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
Db	1501	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	1560
Qy	961	CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCCACTTCCAGCTTCTGAAGA	1020
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Qy      1201  TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
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Db      1801  TCCTGTAGCA-GCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1859
Qy      1261  ACCCTGCAG 1269
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Db      1860  ACCCTGCAG 1868

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RESULT 8

AF136896

LOCUS AF136896 2528 bp mRNA linear MAM 27-FEB-2001

DEFINITION Sus scrofa alpha-1,2-fucosyltransferase (FUT1) mRNA, complete cds.

ACCESSION AF136896

VERSION AF136896.1 GI:7328563

KEYWORDS

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 2528)

AUTHORS Meijerink,E., Neuenschwander,S., Fries,R., Dinter,A.,
Bertschinger,H.U., Stranzinger,G. and Vogeli,P.

TITLE A DNA polymorphism influencing alpha(1,2)fucosyltransferase
activity of the pig FUT1 enzyme determines susceptibility of small
intestinal epithelium to Escherichia coli F18 adhesion

JOURNAL Immunogenetics 52 (1-2), 129-136 (2000)

PUBMED 11132149

REFERENCE 2 (bases 1 to 2528)

AUTHORS Meijerink,E., Neuenschwander,S., Stranzinger,G. and Vogeli,P.

TITLE Direct Submission

JOURNAL Submitted (24-MAR-1999) Institute of Animal Science, Federal
Institute of Technology, Tannenstrasse 1, Zurich, CH 8092,
Switzerland

FEATURES

source

Location/Qualifiers

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/mol_type="mRNA"

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CDS

92. .1189

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ORIGIN

Query Match 98.1%; Score 1245; DB 14; Length 2528;
Best Local Similarity 99.5%; Pred. No. 6.4e-308;
Matches 1259; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy	5	AGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTT	64
Db	88	AGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTT	147
Qy	65	AGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCT	124
Db	148	AGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCT	207
Qy	125	GGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGG	184
Db	208	GGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGG	267
Qy	185	CACGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTTCCGG	244
Db	268	CACGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTTCCGG	327
Qy	245	GACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCT	304
Db	328	GACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCT	387
Qy	305	GCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCCGT	364
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Qy	365	CCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTTGGCGCCCGAGGTAGACAGGCACGC	424
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Qy	425	TCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGA	484
Db	508	TCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGA	567
Qy	485	GCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGA	544
Db	568	GCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGA	627
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Db	628	GCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTACT	687
Qy	605	GAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGT	664
Db	688	GAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGT	747
Qy	665	GCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGG	724
Db	748	GCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGATGG	807
Qy	725	CCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTTGT	784
Db	808	CGCTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTTGT	867

Qy	785	GGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGT	844
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Qy	905	GTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGG	964
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Qy	965	TGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGATCTT	1024
Db	1048	TGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGATCTT	1107
Qy	1025	TAAACCCGAGGCTGCCTTCCTGCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACT	1084
Db	1108	TAAACCCGAGGCTGCCTTCCTGCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACT	1167
Qy	1085	CCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTCAACC	1144
Db	1168	CCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTCAACC	1227
Qy	1145	CAGGGCCAGCGTTATGGGTCTCCGGAAGCCCAGTAACCTCCGGAGATGCTGGTGGTCCT	1204
Db	1228	CAGGGCCAGCGTTATGGGTCTCCGGAAGCCCAGTAACCTCCGGAGATGCTGGTGGTCCT	1287
Qy	1205	GTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAAACCC	1264
Db	1288	GTAGCA-GCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAAACCC	1346
Qy	1265	TGCAG	1269
Db	1347	TGCAG	1351

RESULT 9

AX029029

LOCUS AX029029 1098 bp DNA linear PAT 16-SEP-2000

DEFINITION Sequence 3 from Patent WO9805768.

ACCESSION AX029029

VERSION AX029029.1 GI:10190018

KEYWORDS

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE

1

AUTHORS Mckenzie, I.F. and Sandrin, M.S.

TITLE Improved nucleic acids encoding a chimeric glycosyltransferase

JOURNAL Patent: WO 9805768-A 3 12-FEB-1998;

AUSTIN RESEARCH INST (AU) ; MCKENZIE IAN FARQUHAR CAMPBELL (AU) ; SANDRIN MAURO SERGIO (AU)

FEATURES

source

Location/Qualifiers

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http://es/ScoreAccessWeb/GetItem.action?AppId=09844268&seqId=824812&ItemName=u... 11/15/06

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Qy	969	GATACCATCTACTTGGCTAACTTCACCCTGCCCACCTTCAGCTTCCTGAAGATCTTTAAA	1028
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Db	1081	ATGTTGGCTGGGCCTTGA	1098

RESULT 10

AC168093/c

LOCUS AC168093 199471 bp DNA linear HTG 24-JAN-2006
 DEFINITION Bos taurus clone CH240-234F5, WORKING DRAFT SEQUENCE, 18 unordered pieces.

ACCESSION AC168093
 VERSION AC168093.3 GI:85678869
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE Bos taurus (cattle)

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 199471)

AUTHORS Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P., Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R., Beraducci,A., Biswalo,K., Blyth,P., Bonham,H., Buhay,C., Burch,P., Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I., Chacko,J., Chahrour,M., Chavez,D., Chen,A., Chen,G., Chen,R., Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A., Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Durbin,K., Dziuda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M., Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P., Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T., Gaskin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D., Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeberlen,K., Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Havlak,P., Hawes,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J., Hines,S., Hitchens,M., Hodgson,A., Hogues,M., Hollins,B., Howell,L.T., Hulyk,S., Hume,J., Imo,K., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Kalafus,K., Kelly,S., Keys,T., Khan,Z., King,L., Kovar,C., Kowis,A., Kowis,C., Lara,F., Leal,S., Lee,K., Lee,S., LeGall,F.I., Lemon,S., Lewis,L., Li,B., Li,Y., Li,Z., Linnell,M., Liu,W., Liu,Y.-S., Liu,Y., Liyanage,D., London,P., Lopez,J., Lorensuhewa,L., Lozado,R., Luk,T., Madu,R., Maheshwari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E., McClelland,H., McPherson,J., Mercadao,C., Metzker,M.,

Milosavljevic,A., Minja,E., Morgan,M., Morris,S., Munidas,M.,
Murray,D., Nazarith,L., Ngo,D., Nguyen,N., Norwig-Eastaugh,E.,
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Rabata,D., Rachlin,E., Reigh,R., Ren,Y., Reuter,M., Richards,S.,
Rives,C., Rodriguez,F., Rojas,A., Ruiz,S.J., Sana,M., Sanders,W.,
Santibanez,J., Santos,R., Savery,G., Scherer,S., Shen,H., Shen,Y.,
Sisson,I., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R.,
Svatek,A., Taylor,E., Taylor,T., Thomas,N., Thorn,R., Thornton,R.,
Tremos,Z., Usmani,K., Vargo,C., Verduzco,D., Villasana,D., Virk,D.,
Volkov,A., Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,J.,
Wei,X., Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R.,
Wu,J., Yakub,S., Yan,K., Yuan,Y., Yu,F., Zhang,J., Zhang,L.,
Zhang,Z., Zhou,J., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 199471)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (12-SEP-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 199471)
AUTHORS .
CONSRM Bovine Genome Sequencing Consortium
TITLE Direct Submission
JOURNAL Submitted (24-JAN-2006) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Jan 24, 2006 this sequence version replaced gi:74474967.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: FMZS
Center clone name: CH240-234F5

----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 191995 bases at least Q40
Consensus quality: 193265 bases at least Q30
Consensus quality: 194517 bases at least Q20
Estimated insert size: 197846; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 18 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 43939: contig of 43939 bp in length
 * 43940 43989: gap of 50 bp
 * 43990 47481: contig of 3492 bp in length
 * 47482 47531: gap of 50 bp
 * 47532 82917: contig of 35386 bp in length
 * 82918 82967: gap of 50 bp
 * 82968 84638: contig of 1671 bp in length
 * 84639 84688: gap of 50 bp
 * 84689 94185: contig of 9497 bp in length
 * 94186 94235: gap of 50 bp
 * 94236 106647: contig of 12412 bp in length
 * 106648 106697: gap of 50 bp
 * 106698 115377: contig of 8680 bp in length
 * 115378 115427: gap of 50 bp
 * 115428 155940: contig of 40513 bp in length
 * 155941 155990: gap of 50 bp
 * 155991 165469: contig of 9479 bp in length
 * 165470 165519: gap of 50 bp
 * 165520 167201: contig of 1682 bp in length
 * 167202 167251: gap of 50 bp
 * 167252 171689: contig of 4438 bp in length
 * 171690 171739: gap of 50 bp
 * 171740 182819: contig of 11080 bp in length
 * 182820 182869: gap of 50 bp
 * 182870 188368: contig of 5499 bp in length
 * 188369 188599: gap of 231 bp
 * 188600 192002: contig of 3403 bp in length
 * 192003 193346: gap of 1344 bp
 * 193347 194706: contig of 1360 bp in length
 * 194707 194806: gap of unknown length
 * 194807 195984: contig of 1178 bp in length
 * 195985 196084: gap of unknown length
 * 196085 197474: contig of 1390 bp in length
 * 197475 197574: gap of unknown length
 * 197575 199471: contig of 1897 bp in length.

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gap	82918. .82967 /estimated_length=50
gap	84639. .84688 /estimated_length=50
gap	94186. .94235 /estimated_length=50
gap	106648. .106697

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ORIGIN

Query Match 68.6%; Score 871; DB 12; Length 199471;
 Best Local Similarity 83.3%; Pred. No. 2.6e-212;
 Matches 1050; Conservative 0; Mismatches 205; Indels 6; Gaps 5;

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Qy      1 CTCGAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
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Db      81900 CTGCAGCCATGTGGGCTCCCGGCCACCGTCACCTCTGTCTGATCTTCCTGCTAACCTGTG 81841

Qy      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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Db      81840 TTTTTCGCTGCGTCTTCTTCCTCCTCATCCACCAAACCTCTTTTACAGTGGCTTAGACC 81781

Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATAATTCTGCCTGG 180
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Db      81780 TGTTCCTGCTGTGTCCAGACCGTAGCCGGGTGAGATCCCCCGTGGCCATCCTTTGCCTGT 81721

Qy      181 CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT 240
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Db      81720 CAGGCACACCGATGAACCCCAATGCCACCTTTACCTGTCCAGGCATTCTGCTTCTGTCT 81661

Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
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Db      81660 CAGGAACCTGGACTATCGACCCCAAGGCCGGTTTGGGAACCAGATGGGGCAGTACGCCA 81601

Qy      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
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Qy      421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
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http://es/ScoreAccessWeb/GetItem.action?AppId=09844268&seqId=824812&ItemName=u... 11/15/06

Query Match 64.9%; Score 823.6; DB 14; Length 1083;
Best Local Similarity 85.2%; Pred. No. 7.8e-200;
Matches 919; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

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QY      729 TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTTGTGGTC 788
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QY      849 TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCACTGC 908
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QY      909 AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA 968
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QY      969 GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTCTGAAGATCTTTAAA 1028
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Db      961 GACACCATCTACCTGGCCAACTTCACCCTGCCTGATTCCAGCTTCTCTGAAGATCTTTAAA 1020
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QY      1029 CCCGAGGCTGCCTTCCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCA 1087
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RESULT 13

AR075308

LOCUS AR075308 8174 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 5 from patent US 5955347.

ACCESSION AR075308

VERSION AR075308.1 GI:10002058

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 8174)

AUTHORS Lowe, J.B.

TITLE Methods and products for the synthesis of oligosaccharide structures on glycoproteins, glycolipids, or as free molecules, and for the isolation of cloned genetic sequences that determine these structures

JOURNAL Patent: US 5955347-A 5 21-SEP-1999;

FEATURES Location/Qualifiers

source 1. .8174

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ORIGIN

Query Match 63.7%; Score 808.6; DB 2; Length 8174;

Best Local Similarity 79.6%; Pred. No. 4.1e-196;

Matches 993; Conservative 0; Mismatches 249; Indels 5; Gaps 3;

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QY      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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QY	361	CCGTCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
Db	5038	CCGCCCTGGCCCCGGTATTCCGCGATCACCTGCCCGTGTCTGGCCCCAGAAGTGGACAGCC	5097
QY	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
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QY	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
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QY	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
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QY	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
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QY	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	5458	TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCG	5517
QY	841	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
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QY	1081	CACTCCAGATGTTGGCTGGGCCCTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
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Query Match 63.7%; Score 808.6; DB 5; Length 8549;
 Best Local Similarity 79.6%; Pred. No. 4.1e-196;
 Matches 993; Conservative 0; Mismatches 249; Indels 5; Gaps 3;

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Search completed: November 14, 2006, 04:49:39
Job time : 7446 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 09844268 and Search Result us-09-844-268-12.rng.

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OM nucleic - nucleic search, using sw model

Run on: November 13, 2006, 16:38:38 ; Search time 885 Seconds
(without alignments)
9997.495 Million cell updates/sec

Title: US-09-844-268-12
Perfect score: 1269
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
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- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
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- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	1269	100.0	1269	2	AAX15872	Aax15872 Fragment
	3	1269	100.0	1269	3	AAZ94417	Aaz94417 Pig alpha
	4	1264.2	99.6	1269	6	AAI72831	Aai72831 FUT1 cDNA
	5	1245.8	98.2	3315	11	ADO58598	Ado58598 Porcine a
	6	1094.8	86.3	1098	2	AAV21640	Aav21640 Pig H tra
	7	808.6	63.7	8174	2	AAQ13332	Aaq13332 GDP-Fuc:b
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	14	794.2	62.6	1174	3	AAA53820	Aaa53820 Human H-t
	15	792.2	62.4	3791	2	AAT63575	Aat63575 Chicken b
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	17	789	62.2	1155	2	AAQ98461	Aaq98461 GDP-L-fuc
	18	789	62.2	1155	2	AAT01083	Aat01083 2-Alpha-f
	19	789	62.2	2268	2	AAT63576	Aat63576 Mouse H2K
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	22	454.2	35.8	1043	2	AAV21639	Aav21639 Pig secre
	23	449.4	35.4	3088	6	ABL66311	Abl66311 Lung canc
	24	449.4	35.4	3088	6	ABL70026	Abl70026 Pancreas
	25	449.4	35.4	3088	6	ABL64735	Abl64735 Lung canc
	26	447.8	35.3	2115	2	AAV58323	Aav58323 Human Sec
	27	446.8	35.2	1041	13	ADQ83703	Adq83703 Human tum
	28	446.8	35.2	1041	13	ADQ85849	Adq85849 Human tum
	29	427.8	33.7	2000	12	ADQ83704	Adq83704 Human tum
	30	427.8	33.7	2000	13	ADQ85850	Adq85850 Human tum
	31	423.8	33.4	1068	3	AAC67966	Aac67966 Rat hepat
	32	423.8	33.4	1068	6	AAD27208	Aad27208 Rat hepat
	33	423.8	33.4	1068	8	ABS57887	Abs57887 Rat cDNA
	34	423.8	33.4	1149	3	AAC67965	Aac67965 Rat hepat
	35	423.8	33.4	1149	6	AAD27207	Aad27207 Rat hepat
	36	423.8	33.4	1149	8	ABS57886	Abs57886 Rat cDNA
	37	422.2	33.3	1150	10	ADB97787	Adb97787 Rat cDNA
	38	420.6	33.1	1069	10	ADB97783	Adb97783 Rat cDNA
	39	415.2	32.7	556	12	ACH70096	Ach70096 Human gen
c	40	399	31.4	954	12	ACH89801	Ach89801 Human gen
	41	325.2	25.6	434	12	ACH83796	Ach83796 Human gen
	42	309.4	24.4	1071	2	AAX77268	Aax77268 X. laevis
	43	253	19.9	401	10	ABZ84527	Abz84527 Toxicolog
c	44	129.4	10.2	509	12	ACH76100	Ach76100 Human gen
	45	85.8	6.8	473	3	AAC03536	Aac03536 Human sec

ALIGNMENTS

RESULT 1
AAX03811

ID AAX03811 standard; DNA; 1269 BP.
 XX
 AC AAX03811;
 XX
 DT 01-APR-1999 (first entry)
 XX
 DE Swine alpha-1,2-fucosyltransferase 1 encoding DNA.
 XX
 KW Swine; pig; alpha-1,2-fucosyltransferase 1; FUT1; resistance;
 KW Escherichia coli; infection; oedema; postweaning diarrhoea;
 KW intestinal disorder; polymorphism; ss.
 XX
 OS Sus scrofa.
 XX
 FH Key Location/Qualifiers
 FT CDS 9..1106
 FT /*tag= a
 XX
 PN WO9853102-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US010318.
 XX
 PR 20-MAY-1997; 97US-0047181P.
 XX
 PA (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
 PA (USDA) US SEC OF AGRIC.
 PA (SWTE-) SWISS FEDERAL INST TECHNOLOGY ZURICH.
 XX
 PI Bosworth BT, Vogeli P;
 XX
 DR WPI; 1999-059746/05.
 DR P-PSDB; AAW30630.
 XX
 PT New method of identifying swine that are resistant to intestinal
 PT colonisation by Escherichia coli - comprises use of genetic polymorphic
 PT markers, used for breeding swine resistant to Escherichia coli-related
 PT diseases.
 XX
 PS Claim 6; Fig 1; 35pp; English.
 XX
 CC A method has been developed for the identification of swine that are
 CC resistant to intestinal colonisation by E. coli. The method comprises
 CC determining whether a genetic polymorphism associated with resistance to
 CC colonisation is present in a swine sample, and then inferring that the
 CC swine is resistant if it is homozygous for the polymorphism. The method
 CC uses the swine alpha-1,2-fucosyltransferase (FUT1) polymorphism. The
 CC present sequence encodes swine FUT1. The method enables the breeding of
 CC swine that are resistant to E. coli-related diseases. This method
 CC comprises breeding swine that have a genetic polymorphism in the FUT1
 CC gene. More particularly, the identification method identifies swine that
 CC are resistant to E. coli-related intestinal disorders if, in a sample
 CC taken, the only nitrogen base at residue 307 in the FUT1 gene is adenine.
 CC Larger amplified fragments from the assay can be used for RFLP analysis,
 CC and the assay itself is used as a basis for a kit, applied to swine of
 CC any age, in detecting polymorphisms associated with E. coli F18
 CC receptors. The polymorphisms are useful in developing drugs to treat
 CC swine with E. coli-related diseases. However, a mutated form of the
 CC porcine FUT1 gene may interfere with the normal enzyme and prevent it
 CC from producing the intestinal receptor for F18. The detection of

CC polymorphic markers in the method disclosed enables the detection and
 CC treatment of E. coli-related intestinal diseases in swine, where there
 CC has been no success using antibiotics due to unsuccessful prophylaxis
 XX
 SQ Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 U; 0 Other;

Query Match 100.0%; Score 1269; DB 2; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 3.8e-285;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
Db	1	CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
Qy	61	TTTGTAGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
Db	61	TTTGTAGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
Qy	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Db	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Qy	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT	240
Db	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT	240
Qy	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Db	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Qy	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACG	360
Db	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACG	360
Qy	361	CCGTCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
Db	361	CCGTCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
Qy	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Db	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Qy	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Qy	541	GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Db	541	GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Qy	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Qy	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Qy	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGCTCT	780
Db	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGCTCT	780

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Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
      |||
Db      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840

Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGCGCTGCTGG 900
      |||
Db      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGCGCTGCTGG 900

Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
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Db      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960

Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA 1020
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Qy      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
      |||
Db      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080

Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC 1140
      |||
Db      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC 1140

Qy      1141 AACCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
      |||
Db      1141 AACCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200

Qy      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
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Db      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy      1261 ACCCTGCAG 1269
      |||
Db      1261 ACCCTGCAG 1269

```

RESULT 2

AAX15872

ID AAX15872 standard; DNA; 1269 BP.

XX

AC AAX15872;

XX

DT 13-MAY-1999 (first entry)

XX

DE Fragment of pHT83xF encoding swine alpha(1,2) fucosyltransferase.

XX

KW Swine alpha(1,2) fucosyltransferase; FUT1; Escherichia coli; resistant;

KW E. coli-associated intestinal disorder; E coli infection; ss.

XX

OS Synthetic.

OS Sus sp.

XX

FH Key Location/Qualifiers

FT CDS 9..1106

FT /*tag= a

XX

PN WO9853101-A2.

XX

PD 26-NOV-1998.

XX
 PF 20-MAY-1998; 98WO-US010259.
 XX
 PR 20-MAY-1997; 97US-0047181P.
 XX
 PA (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
 XX
 PI Bosworth BT;
 XX
 DR WPI; 1999-131692/11.
 DR P-PSDB; AAW97356.
 XX
 PT identifying swine genetically resistant to E. coli associated diseases -
 PT using PCR-RFLP to assay for polymorphisms in the alpha(1,2)
 PT fucosyltransferase 1 gene.
 XX
 PS Claim 6; Fig 1; 19pp; English.
 XX
 CC The present sequence encodes swine alpha(1,2) fucosyltransferase (FUT1).
 CC The specification describes methods relating to Escherichia coli-
 CC resistant swine. One of the methods for identifying a swine resistant to
 CC E. coli-associated intestinal disorders, comprises determining whether
 CC the base at 307 of alpha(1,2) fucosyltransferase 1 gene (FUT1) is adenine
 CC (sic), in which case the swine are resistant. The porcine FUT1
 CC polymorphisms can be used to develop drugs for the treatment of swine
 CC having E. coli-associated disease. The methods can also be used in
 CC breeding programmes to identify swine with resistance to E coli infection
 XX
 SQ Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 U; 0 Other;

Query Match 100.0%; Score 1269; DB 2; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 3.8e-285;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTCGAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
Db	1	CTCGAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
QY	61	TTTTCAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
Db	61	TTTTCAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
QY	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Db	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
QY	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT	240
Db	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT	240
QY	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Db	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
QY	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
Db	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
QY	361	CCGTCCTGGCCCCCGTGTTCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC	420
Db	361	CCGTCCTGGCCCCCGTGTTCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC	420

Qy	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Db	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Qy	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Qy	541	GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Db	541	GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Qy	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Qy	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Qy	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
Db	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
Qy	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Qy	841	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
Db	841	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
Qy	901	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
Db	901	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
Qy	961	CTGGTGGAGATAACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA	1020
Db	961	CTGGTGGAGATAACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA	1020
Qy	1021	TCTTTAAACCCGAGGCTGCCTTCTTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Db	1021	TCTTTAAACCCGAGGCTGCCTTCTTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Qy	1081	CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Db	1081	CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Qy	1141	AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG	1200
Db	1141	AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG	1200
Qy	1201	TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Db	1201	TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Qy	1261	ACCCTGCAG	1269
Db	1261	ACCCTGCAG	1269

RESULT 3
AAZ94417
ID AAZ94417 standard; DNA; 1269 BP.
XX
AC AAZ94417;
XX
DT 18-JUL-2000 (first entry)
XX
DE Pig alpha-1-2 fucosyltransferase FUT1 gene.
XX
KW Alpha-1-2 fucosyltransferase; FUT1; pig; polymorphism; Escherichia coli;
KW resistance; ss.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 9..1106
FT /*tag= a
FT /transl_except= (pos:726..728, aa:Ala)
FT variation replace(315,A)
FT /*tag= b
FT /note= "adenine is substituted for guanine in resistant
FT pigs"
XX
PN WO200016641-A1.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-US021408.
XX
PR 18-SEP-1998; 98US-00151592.
XX
PA (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
PA (USDA) US SEC OF AGRIC.
XX
PI Bosworth BT, Ridpath J, Wiseman B;
XX
DR WPI; 2000-283404/24.
DR P-PSDB; AAY79302.
XX
PT Improving weight gain in swine using swine genetically resistant
PT Escherichia coli and feeding swine high levels of plant based protein.
XX
PS Disclosure; Fig 1; 33pp; English.
XX
CC This is the nucleotide sequence of the pig FUT1 gene encoding alpha-1-2
CC fucosyltransferase (see AAY79302). A polymorphism at position 307 of the
CC coding region is associated with susceptibility to F18 Escherichia coli
CC colonization; pigs homozygous for adenine at position 307 are resistant
CC to colonization, while heterozygous animals and animals homozygous for
CC guanine at position 307 are susceptible to colonization. A claimed method
CC for improving weight gain in pigs involves selecting animals that are
CC genetically resistant to E. coli colonization and feeding these animals
CC high levels of plant-based protein concentrate. A claimed method for
CC preventing F18 E. coli colonization in swine, especially swine that are
CC genetically susceptible to F18 E. coli colonization, involves replacing
CC some or all of the plant-based proteins in the diet with animal-based
CC proteins. The polymorphism in the FUT1 gene is also useful for developing
CC drugs to treat swine that have E. coli associated disease. The
CC polymorphism can be detected using PCR-RFLP tests (see also AAZ94418-19)

XX

SQ Sequence 1269 BP; 219 A; 413 C; 362 G; 275 T; 0 U; 0 Other;

Query Match 100.0%; Score 1269; DB 3; Length 1269;
Best Local Similarity 100.0%; Pred. No. 3.8e-285;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
Db	1	CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
Qy	61	TTTGTAGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
Db	61	TTTGTAGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
Qy	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Db	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Qy	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT	240
Db	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT	240
Qy	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Db	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Qy	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACG	360
Db	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACG	360
Qy	361	CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
Db	361	CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
Qy	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Db	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Qy	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Qy	541	GGGAGCAGATCCGCAGCGAGTTCACCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Db	541	GGGAGCAGATCCGCAGCGAGTTCACCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Qy	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Qy	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Qy	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGCTCT	780
Db	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGCTCT	780
Qy	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840

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Db      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGA 1020
Qy      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
Qy      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
Qy      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
Qy      1261 ACCCTGCAG 1269
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Db      1261 ACCCTGCAG 1269

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RESULT 4

AAI72831

ID AAI72831 standard; cDNA; 1269 BP.

XX

AC AAI72831;

XX

DT 22-JUL-2002 (first entry)

XX

DE FUT1 cDNA.

XX

KW Gene; pig; swine; alpha (1,2) fucosyltransferase; FUT1; weight gain; F18;

KW Escherichia coli; ss.

XX

OS Sus scrofa.

XX

FH Key Location/Qualifiers

FT CDS 9. .1106

FT /*tag= a

FT /product= "FUT1"

FT mutation 315

FT /*tag= b

FT /phenotype= "Confers resistance to F18 E. coli"

XX

PN US6355859-B1.

XX

PD 12-MAR-2002.

XX
 PF 18-SEP-1998; 98US-00151592.
 XX
 PR 20-MAY-1997; 97US-0047181P.
 XX
 PA (BIOT-) BIOTECHNOLOGY RES & DEV CORP.
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Bosworth B, Ridpath J, Wiseman B;
 XX
 DR WPI; 2002-391652/42.
 DR P-PSDB; AAB47995.
 XX
 PT Feeding swine genetically susceptible to F18 Escherichia coli
 PT colonization with a low plant protein based diet increases weight gain
 PT and lowers intestinal disease associated with E. coli infection.
 XX
 PS Claim 1; Col 13-18; 9pp; English.
 XX
 CC This sequence represents the swine alpha (1,2) fucosyltransferase (FUT1)
 CC gene. A FUT1 gene in which there is a base other than adenine at position
 CC 307, may be used for improving weight gain in swine that are genetically
 CC susceptible to F18 Escherichia coli. The weight gain may be activated by
 CC feeding a diet of at least 40% animal based proteins. The feeding method
 CC is used to control F18 E. coli associated intestinal disease in swine
 XX
 SQ Sequence 1269 BP; 219 A; 414 C; 361 G; 275 T; 0 U; 0 Other;

Query Match 99.6%; Score 1264.2; DB 6; Length 1269;
 Best Local Similarity 99.8%; Pred. No. 5e-284;
 Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
Db	1	CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
QY	61	TTTGTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
Db	61	TTTGTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
QY	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Db	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
QY	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCTGCCTCCTTTT	240
Db	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCTGCCTCCTTTT	240
QY	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Db	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
QY	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
Db	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
QY	361	CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
Db	361	CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
QY	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480

Db	421		ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Qy	481		AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Db	481		AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540
Qy	541		GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Db	541		GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Qy	601		TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	601		TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Qy	661		ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	661		ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Qy	721		ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
Db	721		ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
Qy	781		TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	781		TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Qy	841		ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
Db	841		ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
Qy	901		TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCGCCTACCTGG	960
Db	901		TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCGCCTACCTGG	960
Qy	961		CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCCACTTCCAGCTTCTGAAGA	1020
Db	961		CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCCACTTCCAGCTTCTGAAGA	1020
Qy	1021		TCTTTAAACCCGAGGCTGCCTTCCGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Db	1021		TCTTTAAACCCGAGGCTGCCTTCCGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Qy	1081		CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC	1140
Db	1081		CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC	1140
Qy	1141		AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCCAGTAAGTTCGGGAGATGCTGGTGG	1200
Db	1141		AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCCAGTAAGTTCGGGAGATGCTGGTGG	1200
Qy	1201		TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Db	1201		TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Qy	1261		ACCCTGCAG 1269	
Db	1261		ACCCTGCAG 1269	

RESULT 5

ADO58598
 ID ADO58598 standard; DNA; 3315 BP.
 XX
 AC ADO58598;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Porcine alpha-1,2-fucosyltransferase (FUT1) DNA.
 XX
 KW Detection method; resistance gene; porcine; epidemic diarrhoea;
 KW Escherichia coli F18 receptor; alpha-1; 2-fucosyltransferase; FUT1; pig;
 KW ds.
 XX
 OS Sus scrofa.
 XX
 PN KR2002080504-A.
 XX
 PD 26-OCT-2002.
 XX
 PF 11-APR-2001; 2001KR-00019282.
 XX
 PR 11-APR-2001; 2001KR-00019282.
 XX
 PA (CHOK/) CHO K K.
 PA (CHOI/) CHOI Y J.
 PA (LEES/) LEE S H.
 XX
 PI Cho KK, Choi YJ, Kim CU, Lee SH;
 XX
 DR WPI; 2003-325954/31.
 XX
 PT Detection of resistance gene against porcine epidemic diarrhea.
 XX
 PS Disclosure; Fig 1; 12pp; Korean.
 XX
 CC The present invention relates to a method of detection of a resistance
 CC gene against porcine epidemic diarrhoea by examining resistance and
 CC susceptibility against Escherichia coli F18 receptor. The detection
 CC involves preparing primers for detecting a mutation of the FUT1 gene, and
 CC detecting a pig, which shows resistance against porcine epidemic
 CC diarrhoea, by PCR using the prepared primers and a test sample collected
 CC from a pig. Also disclosed are sequences of the primers used for the
 CC detection. The present sequence represents porcine FUT1 DNA.
 XX
 SQ Sequence 3315 BP; 648 A; 991 C; 901 G; 775 T; 0 U; 0 Other;

Query Match 98.2%; Score 1245.8; DB 11; Length 3315;
 Best Local Similarity 99.4%; Pred. No. 1.2e-279;
 Matches 1261; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Qy	1	CTCGAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
Db	601	CTGCAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	660
Qy	61	TTTtagcagcaattttcttcctgaacgtctatcaagacctcttttacagtggttagacc	120
Db	661	TTTtagcagcaattttcttcctgaacgtctatcaagacctcttttacagtggttagacc	720
Qy	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Db	721	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	780


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Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1740

Qy      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAAC TTCCGGAGATGCTGGTGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAAC TTCCGGAGATGCTGGTGG 1800

Qy      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      1801 TCCTGTAGCA-GCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1859

Qy      1261 ACCCTGCAG 1269
          |||||||||
Db      1860 ACCCTGCAG 1868
    
```

RESULT 6

AAV21640

ID AAV21640 standard; cDNA; 1098 BP.

XX

AC AAV21640;

XX

DT 08-JUL-1998 (first entry)

XX

DE Pig H transferase encoding cDNA.

XX

KW Pig; H transferase; chimeric; glycosyltransferase; gene therapy;
KW transplantation; ss.

XX

OS Sus scrofa.

XX

FH	Key	Location/Qualifiers
FT	CDS	1. .1098
FT		/*tag= a
FT		/product= "H transferase"

XX

PN WO9805768-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-AU000492.

XX

PR 02-AUG-1996; 96AU-00001402.

PR 21-AUG-1996; 96US-0024279P.

XX

PA (AUST-) AUSTIN RES INST.

XX

PI Mckenzie IFC, Sandrin MS;

XX

DR WPI; 1998-159170/14.

DR P-PSDB; AAW53102.

XX

PT Nucleic acids encoding chimeric glycosyltransferases - used for altering
PT carbohydrate levels on the surface of cells, useful in gene therapy and
PT transplantation.

XX

PS Example 3; Fig 7; 51pp; English.

XX

CC The present sequence encodes pig H transferase used in an example of the
CC present invention. The present invention describes nucleic acids (NA)

CC encoding a chimeric glycosyltransferase. The NAs comprise a catalytic
 CC domain of a first glycosyltransferase (GT) and a localisation signal of a
 CC second GT, whereby when the NA is expressed in a cell and where the
 CC chimeric enzyme is located in an area of the cell where it is able to
 CC compete for substrate with a second GT, resulting in reduced levels of a
 CC product from the second GT. The NAs can be used to produce cells and
 CC organs with desired glycosylation patterns. Products and methods of the
 CC present invention can be used to reduce the levels of undesirable
 CC epitopes in cells, tissues or organs which may be used in transplantation
 CC or gene therapy

XX

SQ Sequence 1098 BP; 181 A; 367 C; 312 G; 238 T; 0 U; 0 Other;

Query Match 86.3%; Score 1094.8; DB 2; Length 1098;
 Best Local Similarity 99.8%; Pred. No. 1.2e-244;
 Matches 1096; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	9	ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA	68
Db	1	ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA	60
Qy	69	GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC	128
Db	61	GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC	120
Qy	129	CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCAGC	188
Db	121	CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCAGC	180
Qy	189	CCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC	248
Db	181	CCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC	240
Qy	249	TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG	308
Db	241	TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG	300
Qy	309	GCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCTCTG	368
Db	301	GCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCTCTG	360
Qy	369	GCCCCCGTGTTCGCGATCAGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCACGCTCCT	428
Db	361	GCCCCCGTGTTCGCGATCAGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCACGCTCCT	420
Qy	429	TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC	488
Db	421	TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC	480
Qy	489	TGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG	548
Db	481	TGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG	540
Qy	549	ATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTACTGAGT	608
Db	541	ATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTACTGAGT	600
Qy	609	CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC	668
Db	601	CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC	660

Qy	669	CGCGGGGACTATCTGCGTGTGATGCCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCCGT	728
Db	661	CGCGGGGACTATCTGCGTGTGATGCCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCGCT	720
Qy	729	TACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCGATACGAAGCCCCGTCTTTGTGGTC	788
Db	721	TACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCGATACGAAGCCCCGTCTTTGTGGTC	780
Qy	789	ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC	848
Db	781	ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC	840
Qy	849	TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAAGTGC	908
Db	841	TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAAGTGC	900
Qy	909	AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA	968
Db	901	AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA	960
Qy	969	GATACCATCTACTTGGCTAACTTCACCTGCCCCACTTCCAGCTTCCTGAAGATCTTTAAA	1028
Db	961	GATACCATCTACTTGGCTAACTTCACCTGCCCCACTTCCAGCTTCCTGAAGATCTTTAAA	1020
Qy	1029	CCCGAGGCTGCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG	1088
Db	1021	CCCGAGGCTGCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG	1080
Qy	1089	ATGTTGGCTGGGCCTTGA	1106
Db	1081	ATGTTGGCTGGGCCTTGA	1098

RESULT 7

AAQ13332

ID AAQ13332 standard; DNA; 8174 BP.

XX

AC AAQ13332;

XX

DT 25-MAR-2003 (revised)

DT 07-NOV-1991 (first entry)

XX

DE GDP-Fuc:beta-D-galactoside alpha(1,2)-fucosyltransferase gene.

XX

KW Glycosyltransferase.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 4686..5783

FT /*tag= a

XX

PN WO9112340-A.

XX

PD 22-AUG-1991.

XX

PF 14-FEB-1990; 90US-00479858.

XX

PR 14-FEB-1990; 90US-00479858.

PR 14-FEB-1990; 90US-00480133.

PR 12-DEC-1990; 90US-00627621.

XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Lowe JB;
 XX
 DR WPI; 1991-267151/36.
 DR P-PSDB; AAR13751.
 XX
 PT Isolation of gene conveying post-translational characteristic - e.g. the
 PT presence of soluble or membrane bound oligo or polysaccharide or
 PT glycosyltransferase.
 XX
 PS Disclosure; Fig 3; 155pp; English.
 XX
 CC The DNA encodes a protein sequence capable of functioning as a GDP-
 CC Fuc:[beta-D-Gal alpha(1,2)- fucosyltransferase. The sequence coded by
 CC nucleotides 4782 - 5780 represents the functional protein. The enzyme
 CC produced by the DNA sequence can be used in enzymatic fucosylation of
 CC chain-terminating galactose residues on lactose- amine or neolacto type
 CC beta-D-galactoside to alpha-2-L-fucose residues. See also AAQ13330-
 CC Q13333. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 8174 BP; 1628 A; 2229 C; 2322 G; 1995 T; 0 U; 0 Other;

Query Match 63.7%; Score 808.6; DB 2; Length 8174;
 Best Local Similarity 79.6%; Pred. No. 7.7e-178;
 Matches 993; Conservative 0; Mismatches 249; Indels 5; Gaps 3;

QY	1	CTCGAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG	60
Db	4678	CTCGAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG	4737
QY	61	TTTTCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC	120
Db	4738	TCCTCTCTGTAATCTTCTTCTCCATATCCATCAAGACAGCTTTCACATGGCCTAGGCC	4797
QY	121	TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG	180
Db	4798	TGTCGATCCTGTGTCCAGACCGCCGCTGGTGACACCCCAAGTGGCCATCTTCTGCCTGC	4857
QY	181	CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT	240
Db	4858	CGGGTACTGCGATGGGCCCAACGCCTCTTCTGTCCCAAGCATCCTGCCTCCTTCT	4917
QY	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Db	4918	CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA	4977
QY	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
Db	4978	CGCTGCTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATG	5037
QY	361	CCGTCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC	420
Db	5038	CCGCCCTGGCCCCGGTATTCCGCATCACCTGCCCCGTGCTGGCCCCAGAAGTGGACAGCC	5097
QY	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Db	5098	GCACGCCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCCGAGGAGTACGCGGACTTGA	5157
QY	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCC	540


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      || || | ||||| | ||||| ||||| ||||| |||||
Db      5158 GAGATCCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCC 5217
Qy      541 GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG 600
      |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5218 GGGAACAGATCCGCAGAGAGTTACCCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTG 5277
Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
      | ||| |||| | ||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      5278 TGCTGGGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTGCGCGTCC 5337
Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5338 ACGTGCGCCGCTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCG 5397
Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5398 ACAGCGCTTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTT 5457
Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5458 TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCG 5517
Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
      | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5518 ATGTGACGTTTGTCTGGCGATGGACAGGAGGCTACACCGTGGAAGACTTTGCCCTGCTCA 5577
Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5578 CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG 5637
Qy      961 CTGGTGGAGATAACCATCTACTTGGCTAACTTCACCCTGCCCACTTCAGCTTCTGAAGA 1020
      |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db      5638 CTGGCGGAGACACTGTCTACCTGGCCAACCTTCACCCTGCCAGACTCTGAGTTCTGAAGA 5697
Qy      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
      ||||| || |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db      5698 TCTTTAAGCCGGAGGCGCCTTCCTGCCCAGTGGGTGGGCATTAATGCAGACTTGTCTC 5757
Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
      |||| | || |||| | |||| | |||| | |||| | || || || || ||
Db      5758 CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC 5815
Qy      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACCTCCGGAGATGCTGGTGG 1200
      | || |||| | || | || | || | || | || | || | || | || | || |
Db      5816 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 5874
Qy      1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
      | || || || || || || || || || || || || || || || || ||
Db      5875 TGTTCTGAAGCAAATGGGTGCCCCTATCCAGAGTGATTCTAGTTGG 5921

```

RESULT 8

AAT61677

ID AAT61677 standard; DNA; 8174 BP.

XX

AC AAT61677;

XX

DT 19-JUN-1997 (first entry)

XX

DE Human alpha(1,2)-fucosyltransferase DNA.

XX
 KW Alpha(1,2)-fucosyltransferase; glycosylation; oligosaccharide;
 KW blood group H; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 4686..5783
 FT /*tag= a
 XX
 PN WO9709421-A1.
 XX
 PD 13-MAR-1997.
 XX
 PF 06-SEP-1996; 96WO-US013816.
 XX
 PR 08-SEP-1995; 95US-00525058.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Lowe JB, Legault DJ;
 XX
 DR WPI; 1997-192897/17.
 DR P-PSDB; AAW13640.
 XX
 PT New recombinant fucosyl:transferase proteins - useful for modifying cell
 PT surface oligosaccharide structures.
 XX
 PS Example 1; Page 274-279; 329pp; English.
 XX
 CC A DNA sequence (AAT61677) codes for human GDP-Fuc:beta-D- galactoside
 CC alpha(1,2)-fucosyltransferase (AAW13640), an enzyme involved in the
 CC expression of type I and II blood group H structures. It was obtd. by
 CC transfecting mouse L cells with DNA derived from human A431 cells, and
 CC selection of transfectants that expressed the H antigen by using anti-H
 CC antibody in a panning procedure. The DNA can be used to construct animal
 CC cell lines with specific capabilities with respect to post-translational
 CC modification of the oligosaccharides of expressed proteins or lipids, or
 CC to produce recombinant enzyme for use in oligosaccharide prodn
 XX
 SQ Sequence 8174 BP; 1628 A; 2229 C; 2322 G; 1995 T; 0 U; 0 Other;

Query Match 63.7%; Score 808.6; DB 2; Length 8174;
 Best Local Similarity 79.6%; Pred. No. 7.7e-178;
 Matches 993; Conservative 0; Mismatches 249; Indels 5; Gaps 3;

QY 1 CTCGAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
 || ||||| ||| ||| || || ||||| ||| ||||| |||||
 Db 4678 CTGCAGCCATGTGGCTCCGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 4737
 QY 61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
 | | | | | ||||| | || ||||| ||| ||| |||
 Db 4738 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCACATGGCCTAGGCC 4797
 QY 121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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 Db 4798 TGTGATCCTGTGTCCAGACCGCCGCTGGTGACACCCAGTGGCCATCTTCTGCCTGC 4857
 QY 181 CGGGCAGCCGGTACACCCCAACGCCTCCGATTCCTGTCCCAAGCATCCTGCCTCCTTTT 240
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 Db 4858 CGGGTACTGCGATGGGCCCAACGCCTCCTTCTTCTGTCCCAAGCATCCTGCCTCCTT 4917

Qy	241	CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA	300
Db	4918	CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA	4977
Qy	301	CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG	360
Db	4978	CGCTGCTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATG	5037
Qy	361	CCGTCTCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTCTGGCGCCCGAGGTAGACAGGC	420
Db	5038	CCGCCCTGGCCCCCGGTATTCCGCGATCACCTGCCCGTGTCTGGCCCCAGAAGTGGACAGCC	5097
Qy	421	ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA	480
Db	5098	GCACGCCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCTGGAGGAGTACGCGGACTTGA	5157
Qy	481	AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGTCTCTGGACCTTCTTCCACCACCTCC	540
Db	5158	GAGATCCTTCTCTGAAGCTCTCTGGCTTCCCCTGTCTCTGGACTTTCTTCCACCATCTCC	5217
Qy	541	GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Db	5218	GGGAACAGATCCGCAGAGAGTTACCCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTG	5277
Qy	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	5278	TGCTGGGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTCTGGCGTCC	5337
Qy	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	5338	ACGTGCGCCGTGGGGACTATCTGCAGGTTATGCCCTCAGCGCTGGAAGGGTGTGGTGGGCG	5397
Qy	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCT	780
Db	5398	ACAGCGCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTTT	5457
Qy	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	5458	TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCG	5517
Qy	841	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG	900
Db	5518	ATGTGACGTTTGTCTGGCGATGGACAGGAGGCTACACCGTGGAAGACTTTGCCCTGCTCA	5577
Qy	901	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCCTACCTGG	960
Db	5578	CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG	5637
Qy	961	CTGGTGGAGATAACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
Db	5638	CTGGCGGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCTGAAGA	5697
Qy	1021	TCTTTAAACCCGAGGCTGCCTTCTTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Db	5698	TCTTTAAGCCGGAGGCGCCTTCTTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	5757
Qy	1081	CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Db	5758	CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC	5815

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Qy      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTCCGGAGATGCTGGTGG 1200
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Db      5816 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 5874

Qy      1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
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Db      5875 TGTTCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 5921
    
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RESULT 9

ACN37237/c

ID ACN37237 standard; DNA; 20001 BP.

XX

AC ACN37237;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human periodontal disease related gene FUT1 SEQ ID NO:147.

XX

KW periodontal disease; polymorphism; ds; human; gene; SNP;

KW single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT		/note= "Variable nucleotide G,A"
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PN  WO2004042054-A1.
XX
PD  21-MAY-2004.
XX
PF  22-OCT-2003; 2003WO-IB004669.

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Db      12312 GAGATCCTTTCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTTCTTCCACCATCTCC 12253

Qy      541 GGGAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG 600
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Db      12252 GGGAACAGATCCGCAGAGAGTTACCCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTG 12193

Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
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Db      12192 TGCTGGGTGAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTGCGCGTCC 12133

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
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Db      12132 ACGTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCG 12073

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
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Db      12072 ACAGCGCTTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTT 12013

Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
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Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
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Db      11952 ATGTGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGAAAGACTTTGCCCTGCTCA 11893

Qy      901 TGCAAGTGAACACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCTACCTGG 960
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Db      11892 CACAGTGAACACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG 11833

Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA 1020
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Qy      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
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Db      11772 TCTTTAAGCCGGAGGCGGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 11713

Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC 1140
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Db      11712 CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC 11655

Qy      1141 AACCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
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Db      11654 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 11596

Qy      1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
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Db      11595 TGTTCCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 11549

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RESULT 10
 AAQ56908
 ID AAQ56908 standard; DNA; 8174 BP.
 XX
 AC AAQ56908;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-JUL-1994 (first entry)
 XX

DE DNA encoding a glycosyltransferase.
 XX
 KW Glycosyltransferase; fucosyltransferase; GDP-Fuc; in vitro; cell;
 KW surface; oligosaccharide; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 4686..5783
 FT /*tag= a
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 PN WO9402616-A1.
 XX
 PD 03-FEB-1994.
 XX
 PF 20-JUL-1993; 93WO-US006703.
 XX
 PR 20-JUL-1992; 92US-00914281.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Lowe JB;
 XX
 DR WPI; 1994-048874/06.
 DR P-PSDB; AAR45936.
 XX
 PT DNA fragment encoding a glycosyltransferase - can be used for in vitro
 PT reactions to modify cell surface oligosaccharide(s) e.g. blood gp.
 PT determinants, to protect against transplant rejection.
 XX
 PS Disclosure; Fig 3; 249pp; English.
 XX
 CC The sequence is that encoding human glycosyl transferase. The enzyme
 CC produced by the DNA may be non glycosylated. This prevents premature loss
 CC of enzyme activity. It can also be used in in vitro reactions to modify
 CC cell surface oligosaccharide mols. e.g. blood group determinants. See
 CC also AAQ56905-12. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 8174 BP; 1628 A; 2228 C; 2322 G; 1996 T; 0 U; 0 Other;

Query Match 63.6%; Score 807; DB 2; Length 8174;
 Best Local Similarity 79.6%; Pred. No. 1.8e-177;
 Matches 992; Conservative 0; Mismatches 250; Indels 5; Gaps 3;

Qy 1 CTCGAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
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 Db 4678 CTGCAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 4737
 Qy 61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
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 Db 4738 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTCCACATGGCCTAGGCC 4797
 Qy 121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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 Db 4798 TGTCGATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCAAGTGGCCATCTTCTGCCTGC 4857
 Qy 181 CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCTGCCTCCTTTT 240
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 Db 4858 CGGGTACTGCGATGGGCCCCAACGCCTCCTCTTCTGTCCCAAGCACCTGCTTCCCTCT 4917
 Qy 241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

Db 5816 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 5874
 Qy 1201 TCCTGTAGCAG--GCTGGACACTTATTTCAGAGTGATTCTAATTGG 1245
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 Db 5875 TGTTCCTGAAGCAAATGGGTGCCCCGTATCCAGAGTGATTCTAGTTGG 5921

RESULT 11

AAT76768

ID AAT76768 standard; cDNA; 3373 BP.

XX

AC AAT76768;

XX

DT 15-SEP-1997 (first entry)

XX

DE Human alpha 1,2 fucosyltransferase cDNA.

XX

KW Human GDP-L-fucose:beta-D-galactoside-2-alpha-L-fucosyltransferase;

KW alpha 1,2 FT; transgene; transgenic mouse; animal model;

KW intestinal adhesion; Helicobacter pylori infection; stomach;

KW small intestine; gut; epithelial cell; surface receptor;

KW carbohydrate antigen; gastritis; peptic ulcer; neoplasia;

KW gastric adenocarcinoma; Lewis antigen; fucosylation; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 104..1201

FT /*tag= a

FT /EC_number= "2.4.1.69"

XX

PN US5625124-A.

XX

PD 29-APR-1997.

XX

PF 11-JUL-1994; 94US-00273411.

XX

PR 11-JUL-1994; 94US-00273411.

XX

PA (UNIW) UNIV WASHINGTON.

XX

PI Falk P, Gordon JI;

XX

DR WPI; 1997-258275/23.

DR P-PSDB; AAW23805.

XX

PT Animal model for Helicobacter pylori infection - comprising transgenic

PT mouse expressing human enzyme promoting intestinal adhesion.

XX

PS Example 1; Col 17-20; 24pp; English.

XX

CC A claimed transgenic mouse expresses, in its intestinal epithelial cells,
 CC the enzyme human GDP-L-fucose:beta-D-galactoside 2-alpha-L-
 CC fucosyltransferase (also called alpha 1,2 FT) or human GDP-L-fucose: beta
 CC -D-N-acetylglucosamide 3/4-alpha-L-fucosyltransferase (also called alpha
 CC 1,3/4 FT). The enzyme is expressed under the control of a gut epithelial
 CC cell-specific promoter and Helicobacter pylori adheres to the transgenic
 CC cells. The transgenic mouse and intestinal epithelial cells from it are
 CC useful as models for screening compounds for the ability to inhibit
 CC adhesion of H. pylori to gut epithelial cells. The present sequence
 CC encodes human alpha 1,2 FT and was published by Larsen et al.,


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Db      881  GTCACCAGCAACGGCATGGAGTGGTGTAAAGAAAACATCGACACCTCCCAGGGCGATGTG 940
QY      846  ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
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Db      941  ACGTTTGTCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 1000
QY      906  TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCGGCCTACCTGGCTGGT 965
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Db      1001 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCACCTGGCTGGC 1060
QY      966  GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCCTCCAGCTTCCTGAAGATCTTT 1025
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Db      1061 GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCTGAAGATCTTT 1120
QY      1026 AAACCCGAGGCTGCCCTTCCTGCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
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Db      1121 AAGCCGGAGGCGGCCCTTCCTGCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1180
QY      1086 CAGATGTTGGCTGGGCTTGAACCCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
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QY      1146 AGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACCTCCGGAGATGCTGGTGGTCTCTG 1205
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QY      1206 TAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
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RESULT 12

AAD46825

ID AAD46825 standard; cDNA; 3373 BP.

XX

AC AAD46825;

XX

DT 27-JAN-2003 (first entry)

XX

DE Human alpha(1,2)fucosyltransferase (alpha1,2FT) cDNA.

XX

KW Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT;

KW transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;

KW gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 104..1201

FT /*tag= a

FT /product= "Human alpha1,2FT protein"

XX

PN WO200274948-A2.

XX

PD 26-SEP-2002.

XX

PF 21-MAR-2002; 2002WO-CA000378.

XX

PR 21-MAR-2001; 2001US-0277811P.

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QY	66	GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG	125
Db	161	TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCACATGGCCTAGGCCTGTCTG	220
QY	126	GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC	185
Db	221	ATCCTGTGTCCAGACCGCCGCTGGTGACACCCAGTGGCCATCTTCTGCCTGCCGGGT	280
QY	186	ACGCCGTTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCTGCCTCCTTTTCCGGG	245
Db	281	ACTGCGATGGGCCCAACGCCTCCTCTTCTGTCCCAAGCATCTGCCTCCTTCTCCGGC	340
QY	246	ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG	305
Db	341	ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG	400
QY	306	CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCCGTC	365
Db	401	CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCCTTTATCTGCCTGCCATGCATGCCGCC	460
QY	366	CTGGCCCCGTTCCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCACGCT	425
Db	461	CTGGCCCCGTTATTCGCATCACCTGCCCGTGTCTGGCCCCAGAAGTGACAGCCGCACG	520
QY	426	CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG	485
Db	521	CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCTGGAGGAGTACGCGGACTTGAGAGAT	580
QY	486	CCCTGGCTGAAGCTCACCGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAG	545
Db	581	CCTTTCTGAAGCTCTCTGGCTTCCCTGCTCTTGGACTTTCTTCCACCATCTCCGGGAA	640

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Qy      546 CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTACTG 605
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Qy      606 AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
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Qy      666 CGCCGCGGGGACTATCTGCGTGTGATGCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
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Db      761 CGCCGTGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 820

Qy      726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCTTTGTG 785
          |||
Db      821 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTCTTCGTG 880

Qy      786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
          |||
Db      881 GTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCGATGTG 940

Qy      846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
          |||
Db      941 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 1000

Qy      906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCTACCTGGCTGGT 965
          |||
Db      1001 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 1060

Qy      966 GGAGATACCATCTACTTGGCTAATTTCACCCTGCCCCTTCCAGCTTCCTGAAGATCTTT 1025
          |||
Db      1061 GGAGACACTGTCTACCTGGCCAATTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1120

Qy      1026 AAACCCGAGGCTGCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
          |||
Db      1121 AAGCCGGAGGCGGCCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1180

Qy      1086 CAGATGTTGGCTGGGCCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
          |||
Db      1181 TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1238

Qy      1146 AGGGCCAGCGTTATGGGTCTCCGGAAGCCCCAGTAACCTCCGGAGATGCTGGTGGTCCCTG 1205
          |||
Db      1239 AGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGGTGTTTC 1297

Qy      1206 TAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
          |||
Db      1298 CTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 1339

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RESULT 13

AAT12238

ID AAT12238 standard; cDNA to mRNA; 1174 BP.

XX

AC AAT12238;

XX

DT 08-APR-1996 (first entry)

XX

DE Human H-transferase cDNA.

XX

KW H-transferase; xenograft hyperacute rejection; transplantation;

QY	6	GCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTA	65
Db	12	GCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTGTCTCTC	71
QY	66	GCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTG	125
Db	72	TCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCACATGGCCTAGGCCTGTCTG	131
QY	126	GCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGC	185
Db	132	ATCCTGTGTCCAGACCGCCGCCTGGTGACACCCCAAGTGGCCATCTTCTGCCTGCCGGGT	191
QY	186	ACGCCGGTACACCCCAACGCCTCCGATTCTCTGTCCCAAGCATCTGCCTCCTTTTCCGGG	245
Db	192	ACTGCGATGGGCCCCAACGCCTCCTCTTCTGTCCCCAGCACCTGCTTCCCTCTCCGGC	251

Qy	246	ACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTG	305
Db	252	ACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGCTG	311
Qy	306	CTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCCGTC	365
Db	312	CTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATGCCGCC	371
Qy	366	CTGGCCCCCGTGTTCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCACGCT	425
Db	372	CTGGCCCCGGTATTCCGCATCACCTGCCCGTGTGGCCCCAGAAGTGACAGCCGCACG	431
Qy	426	CCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAG	485
Db	432	CCGTGGCGGGAGCTGCAGCTTCACGACTGGATGTCCGAGGAGTACGCGGACTTGAGAGAT	491
Qy	486	CCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGGAG	545
Db	492	CCTTTCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTCTTCCACCATCTCCGGGAA	551
Qy	546	CAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCCGAGGGGTTACTG	605
Db	552	CAGATCCGCAGAGAGTTCACCCTGCACGACCACCTTCGGGAAGAGGCCGCAGAGTGTGCTG	611
Qy	606	AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG	665
Db	612	GGTCAGCTCCGCTGGGCCGCACAGGGGACCGCCCGGCACCTTTGTGGCGTCCACGTG	671
Qy	666	CGCCCGGGGGACTATCTGCGTGTGATGCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC	725
Db	672	CGCCGTGGGGACTATCTGCAGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC	731
Qy	726	CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCGTCTTTGTG	785
Db	732	GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTTCCTGTG	791
Qy	786	GTCACCAGCAACGGCATGGAGTGGTGCCGAAGAACATCGACACCTCCCGGGGGACGTG	845
Db	792	GTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCGATGTG	851
Qy	846	ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG	905
Db	852	ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG	911
Qy	906	TGCAACCACACCATCATGACCATTTGGCACCTTCGGCTTCTGGGCCGCCACCTGGCTGGT	965
Db	912	TGCAACCACACCATATGACCATTTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC	971
Qy	966	GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACCTCCAGCTTCCTGAAGATCTTT	1025
Db	972	GGAGACACTGTCTACCTGGCCAACCTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT	1031
Qy	1026	AAACCCGAGGCTGCCTTCTTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC	1085
Db	1032	AAGCCGGAGGCGGCTTCTTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC	1091
Qy	1086	CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC	1145
Db	1092	TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT	1149
Qy	1146	AGGGCCAGCGTTATGGGTCTCCGGA	1170

Db 1150 AGAGCCAGCAGTACGTGGCTTCAGA 1174

RESULT 14

AAA53820

ID AAA53820 standard; cDNA to mRNA; 1174 BP.

XX

AC AAA53820;

XX

DT 03-JAN-2001 (first entry)

XX

DE Human H-transferase coding sequence.

XX

KW mesenchymal stem cell; stem cell; H-transferase; glycosyltransferase;
KW transplantation; xenotransplantation; transgenic animal; tissue injury;
KW bone; joint; tendon; ligament; trauma; tumour infection;
KW muscular dystrophy; osteoarthritis; rheumatoid arthritis; ds.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	CDS	15. .1112
FT		/*tag= a
FT		/product= "H-transferase"

XX

PN WO200049136-A1.

XX

PD 24-AUG-2000.

XX

PF 16-FEB-2000; 2000WO-US003963.

XX

PR 17-FEB-1999; 99US-0120452P.

XX

PA (USSU) US SURGICAL.

XX

PI Gruskin EA, Tawil N, Geis D;

XX

DR WPI; 2000-533106/48.

DR

P-PSDB; AAY97279.

XX

PT Isolated mesenchymal stem cell comprising nucleic acid encoding an immune
PT system suppressor polypeptide, useful for treatment of tissue injuries
PT and/or tissue disorders such as bone and joint fractures.

XX

PS Example 4; Page 40-41; 60pp; English.

XX

CC New methods are described for treating a tissue in need of repair or
CC reconstruction comprising administering a composition comprising a
CC mesenchymal stem cell where the stem cell differentiates into a cell
CC which is normally indigenous to the tissue. The mesenchymal stem cell
CC does not trigger an immune response in the recipient due to it being
CC transfected with a vector comprising nucleic acid which encodes for an
CC immune system repressor polypeptide. The mesenchymal stem cell may be
CC removed from the recipient; transfected and then replaced or derived from
CC a donor transgenic animal. The transfected mesenchymal stem cells are
CC useful for treatment of tissue injuries and/or tissue disorders such as
CC bone and joint fractures, bone defects resulting from trauma, tumour
CC infection, tendon and ligament defects, congenital defects, muscular
CC dystrophy, osteoarthritis, and rheumatoid arthritis. The use of the
CC genetically engineered cells is advantageous because the need for


```

Qy      726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTTGTG 785
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      732 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTTTCGTG 791

Qy      786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      792 GTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCGATGTG 851

Qy      846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      852 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 911

Qy      906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGT 965
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      912 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 971

Qy      966 GGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCCTGAAGATCTTT 1025
          ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      972 GGAGACACTGTCTACCTGGCCAACCTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1031

Qy      1026 AAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
          || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1032 AAGCCGAGGCGGCCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1091

Qy      1086 CAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
          || ||||| ||||| ||||| ||||| || ||||| || |||||
Db      1092 TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1149

Qy      1146 AGGGCCAGCGTTATGGGTCTCCGGA 1170
          || ||||| || || || || ||
Db      1150 AGAGCCAGCAGTACGTGGCTTCAGA 1174
  
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RESULT 15

AAT63575

ID AAT63575 standard; DNA; 3791 BP.

XX

AC AAT63575;

XX

DT 01-JUL-1997 (first entry)

XX

DE Chicken beta-actin promoter.

XX

KW Xenotransplantation; organ transplant; transgenic animal; transgenic pig;

KW transgenic mouse; antibody mediated rejection; hyperacute rejection;

KW antigen reducing enzyme; alpha(1,2)fucosyltransferase; beta-actin;

KW promoter; ss.

XX

OS Gallus sp.

XX

PN WO9712035-A2.

XX

PD 03-APR-1997.

XX

PF 23-SEP-1996; 96WO-US015255.

XX

PR 27-SEP-1995; 95US-0004461P.

PR 03-JUL-1996; 96US-00675773.

XX

PA (NEXT-) NEXTRAN.

XX

Db	2596	CAGATCCGCAGAGAGTTACCCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG	2655
Qy	606	AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG	665
Db	2656	GGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTGCGCGTCCACGTG	2715
Qy	666	CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC	725
Db	2716	CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC	2775
Qy	726	CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCGCTTTTGTG	785
Db	2776	GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGACGGCACGAAGCCCCGCTTTTCGTG	2835
Qy	786	GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGACGTG	845
Db	2836	GTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCGATGTG	2895
Qy	846	ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG	905
Db	2896	ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG	2955
Qy	906	TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCTACCTGGCTGGT	965
Db	2956	TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC	3015
Qy	966	GGAGATACCATCTACTTGGCTAACTTACCCTGCCCCACTTCCAGCTTCCTGAAGATCTTT	1025
Db	3016	GGAGACACTGTCTACCTGGCCAACTTACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT	3075
Qy	1026	AAACCCGAGGCTGCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC	1085
Db	3076	AAGCCGGAGGCGGCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC	3135
Qy	1086	CAGATGTTGGCTGGGCCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC	1145
Db	3136	TGGACATTGGCTAAGCCTTGAGTCGACGTGCAGGCATGCAAGCTTCGGGTGGACCCGGTC	3195
Qy	1146	AGGGCCAGCGTTATGGG	1162
Db	3196	AACTTCAAGGTGAGCGG	3212

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Job time : 890 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 09 and Search Result us-09-844-268-12.rnpb

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This page gives you Search Results detail for the Application 09844268 and Search Result us-09-844-268-12.

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OM nucleic - nucleic search, using sw model

Run on: November 13, 2006, 21:00:25 ; Search time 1815 Seconds
(without alignments)
8591.190 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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3	1094.8	86.3	1098	3	US-09-051-034A-3	Sequence 3, Appli
4	808.6	63.7	8174	3	US-09-863-475A-5	Sequence 5, Appli
5	806.8	63.6	3373	6	US-10-105-963-9	Sequence 9, Appli
6	806.8	63.6	3373	16	US-11-219-419-9	Sequence 9, Appli
7	454.2	35.8	1043	3	US-09-051-034A-1	Sequence 1, Appli
8	454.2	35.8	1043	3	US-09-254-077A-5	Sequence 5, Appli
9	449.4	35.4	3088	3	US-09-954-456-45	Sequence 45, Appl
10	449.4	35.4	3088	3	US-09-954-456-1621	Sequence 1621, Ap
11	449.4	35.4	3088	3	US-09-969-347-234	Sequence 234, App
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41	69.6	5.5	100	6	US-10-040-863-29	Sequence 29, Appl
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ALIGNMENTS

RESULT 1

US-09-844-268-12

; Sequence 12, Application US/09844268

; Patent No. US20020129395A1


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; GENERAL INFORMATION:
; APPLICANT: BOSWORTH, BRAD
; APPLICANT: VOGELI, PETER
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
; TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
; FILE REFERENCE: 21419/90368
; CURRENT APPLICATION NUMBER: US/09/844,268
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/443,766
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Porcine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(1103)
US-09-844-268-12
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Qy     61  TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
        |||
Db     61  TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120

Qy    121  TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
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        |||
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Qy    241  CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
        |||
Db    241  CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

Qy    301  CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
        |||
Db    301  CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

Qy    361  CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
        |||
Db    361  CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420

Qy    421  ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCCACTTAA 480
        |||
Db    421  ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCCACTTAA 480

Qy    481  AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
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Db    481  AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
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Qy	541	GGGAGCAGATCCGCGAGCGAGTTCACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Db	541	GGGAGCAGATCCGCGAGCGAGTTCACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG	600
Qy	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Db	601	TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC	660
Qy	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Db	661	ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG	720
Qy	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
Db	721	ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCT	780
Qy	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Db	781	TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG	840
Qy	841	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCAGGGACTTTGCGCTGCTGG	900
Db	841	ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCAGGGACTTTGCGCTGCTGG	900
Qy	901	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
Db	901	TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG	960
Qy	961	CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
Db	961	CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA	1020
Qy	1021	TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Db	1021	TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC	1080
Qy	1081	CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Db	1081	CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC	1140
Qy	1141	AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG	1200
Db	1141	AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG	1200
Qy	1201	TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Db	1201	TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA	1260
Qy	1261	ACCCTGCAG	1269
Db	1261	ACCCTGCAG	1269

RESULT 2

US-09-844-705-12

; Sequence 12, Application US/09844705

; Patent No. US20020133836A1

; GENERAL INFORMATION:

; APPLICANT: BOSWORTH, BRAD

; APPLICANT: VOGELI, PETER

; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY

```
; TITLE OF INVENTION: RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
; FILE REFERENCE: 21419/90368
; CURRENT APPLICATION NUMBER: US/09/844,705
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/443,766
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Porcine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(1103)
US-09-844-705-12
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Query Match          100.0%; Score 1269; DB 3; Length 1269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
        |||
Db       1 CTCGAGCCATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60

QY     61 TTTTAGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
        |||
Db     61 TTTTAGCAGCAATTTTCTTCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120

QY    121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
        |||
Db    121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180

QY    181 CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT 240
        |||
Db    181 CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT 240

QY    241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
        |||
Db    241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300

QY    301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360
        |||
Db    301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACG 360

QY    361 CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420
        |||
Db    361 CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGC 420

QY    421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
        |||
Db    421 ACGCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAA 480

QY    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
        |||
Db    481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540

QY    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG 600
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Db    541 GGGAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG 600
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Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
        |||
Db      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
        |||
Db      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCGATACGAAGCCCCCGTCT 780
        |||
Db      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCGATACGAAGCCCCCGTCT 780

Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAATCGACACCTCCCGGGGGG 840
        |||
Db      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAATCGACACCTCCCGGGGGG 840

Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGCGCTGCTGG 900
        |||
Db      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGCGCTGCTGG 900

Qy      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960
        |||
Db      901 TGCAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGG 960

Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCTGCCCACTTCCAGCTTCTGAAGA 1020
        |||
Db      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCTGCCCACTTCCAGCTTCTGAAGA 1020

Qy      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
        |||
Db      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080

Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC 1140
        |||
Db      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTCTGGAATAGCCTCGGTC 1140

Qy      1141 AAGCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200
        |||
Db      1141 AAGCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGG 1200

Qy      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260
        |||
Db      1201 TCCTGTAGCAGGCTGGACACTTATTTCAAGAGTGATTCTAATTGGCTGGACTCAGAGGAA 1260

Qy      1261 ACCCTGCAG 1269
        |||
Db      1261 ACCCTGCAG 1269
    
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RESULT 3

US-09-051-034A-3

; Sequence 3, Application US/09051034A

; Patent No. US20010055584A1

; GENERAL INFORMATION:

; APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL

; APPLICANT: SANDRIN, MAURO SERGIO

; TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC

; TITLE OF INVENTION: GLYCOSYLTRANSFERASE

; FILE REFERENCE: 30562.6USWO

; CURRENT APPLICATION NUMBER: US/09/051,034A

; CURRENT FILING DATE: 1998-03-31

```
; PRIOR APPLICATION NUMBER: PCT/AU97/00492
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 60/024,279
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: PO1402
; PRIOR FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Sus Domesticus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1098)
US-09-051-034A-3
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Query Match      86.3%; Score 1094.8; DB 3; Length 1098;
Best Local Similarity 99.8%; Pred. No. 8.5e-313;
Matches 1096; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      9 ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA 68
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGTGGGTCCCCAGCCGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTGTTTTAGCA 60

QY     69 GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC 128
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACCTGCTGGCC 120

QY    129 CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCAGC 188
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGGCGGGCAGC 180

QY    189 CCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC 248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTTCCGGGACC 240

QY    249 TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG 308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTG 300

QY    309 GCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCCGTCTCTG 368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCCGTCTCTG 360

QY    369 GCCCCCGTGTTCCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCACGCTCCT 428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCCCCCGTGTTCCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCACGCTCCT 420

QY    429 TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC 488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCC 480

QY    489 TGGCTGAAGCTCACCGGCTTCCCTTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG 548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGGCTGAAGCTCACCGGCTTCCCTTGCTCCTGGACCTTCTTCCACCACCTCCGGGAGCAG 540

QY    549 ATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTACTGAGT 608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTACTGAGT 600
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Qy	609	CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC	668
Db	601	CAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTGCGC	660
Qy	669	CGCGGGGACTATCTGCGTGTGATGCCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCCGT	728
Db	661	CGCGGGGACTATCTGCGTGTGATGCCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCGCT	720
Qy	729	TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTTGTGGTC	788
Db	721	TACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTTGTGGTC	780
Qy	789	ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC	848
Db	781	ACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATC	840
Qy	849	TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCA GTGC	908
Db	841	TTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCA GTGC	900
Qy	909	AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA	968
Db	901	AACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTGGTGGA	960
Qy	969	GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTTGAAGATCTTTAAA	1028
Db	961	GATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTTGAAGATCTTTAAA	1020
Qy	1029	CCCGAGGCTGCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG	1088
Db	1021	CCCGAGGCTGCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTCCAG	1080
Qy	1089	ATGTTGGCTGGGCCTTGA	1106
Db	1081	ATGTTGGCTGGGCCTTGA	1098

RESULT 4

US-09-863-475A-5

; Sequence 5, Application US/09863475A

; Patent No. US20020102688A1

; GENERAL INFORMATION:

; APPLICANT: LOWE, JOHN B.

; TITLE OF INVENTION: METHODS AND PRODUCTS FOR THE SYNTHESIS

; OF OLIGOSACCHARIDE STRUCTURES ON GLYCOPROTEINS,

; GLYCOLIPIDS, OR AS FREE MOLECULES, AND FOR THE ISOLATION

; OF CLONED GENETIC SEQUENCES THAT DETERMINE THESE STRUCTUR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; P.C.

; STREET: 1755 Jefferson Davis Highway, Fourth Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,475A
; FILING DATE: 24-May-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/914,281
; FILING DATE: 20-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Lavalleye, Jean-Paul M. P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 2363-060-55
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8174 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-863-475A-5

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Query Match 63.7%; Score 808.6; DB 3; Length 8174;
 Best Local Similarity 79.6%; Pred. No. 5.4e-228;
 Matches 993; Conservative 0; Mismatches 249; Indels 5; Gaps 3;

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Qy      1 CTCGAGCCATGTGGGTCCCCAGCCGCCACCTCTGTCTGACCTTCCTGCTAGTCTGTG 60
      || ||||| ||| ||| || || ||||| || ||||| |||||
Db      4678 CTGCAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCCTGCTAGTCTGTG 4737

Qy      61 TTTTAGCAGCAATTTTCTTCCTGAACGTCTATCAAGACCTCTTTTACAGTGGCTTAGACC 120
      | | | | ||| ||||| | || ||||| |||| | ||| |||
Db      4738 TCCTCTCTGTAATCTTCTTCCTCCATATCCATCAAGACAGCTTTCACATGGCCTAGGCC 4797

Qy      121 TGCTGGCCCTGTGTCCAGACCATAACGTGGTATCATCTCCCGTGGCCATATTCTGCCTGG 180
      || | ||||| ||||| | ||| || | ||||| |||||
Db      4798 TGTCGATCCTGTGTCCAGACCGCCGCTGGTGACACCCCCAGTGGCCATCTTCTGCCTGC 4857

Qy      181 CGGGCAGCCGGTACACCCCAACGCCTCCGATTCTGTCCCAAGCATCCTGCCTCCTTTT 240
      |||| || || | ||||| ||||| ||||| ||||| ||||| |||
Db      4858 CGGGTACTGCGATGGGCCCAACGCCTCCTCTTCCTGTCCCCAGCACCTGCTTCCCTCT 4917

Qy      241 CCGGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCA 300
      |||| ||||| || | |||| | ||||| || ||||| ||||| |||||
Db      4918 CCGGCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCA 4977

Qy      301 CGCTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACG 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db      4978 CGCTGCTGGCTCTGGCCCAGCTCAACGGCCGCCGGGCCTTTATCCTGCCTGCCATGCATG 5037

Qy      361 CCGTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGC 420
      ||| ||||| || || ||||| ||||| || ||||| || || |||||
Db      5038 CCGCCCTGGCCCCGGTATTCCGATCACCTGCCCCGTGCTGGCCCCAGAAGTGGACAGCC 5097

Qy      421 ACGCTCCTTGGCGGGAGCTGGAGCTTACGACTGGATGTCCGAGGATTATGCCCACTTAA 480
      | | || ||||| ||||| ||||| ||||| ||||| || || |||||
Db      5098 GCACGCCGTGGCGGGAGCTGCAGCTTACGACTGGATGTCCGAGGAGTACGGGACTTGA 5157

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Qy      481 AGGAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCC 540
      || || | ||||| | ||||| ||||| ||||| ||||| |||||
Db      5158 GAGATCCTTTCCTGAAGCTCTCTGGCTTCCCCTGCTCTTGGACTTCTTCCACCATCTCC 5217

Qy      541 GGGAGCAGATCCGCAGCAGGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGG 600
      |||| | ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      5218 GGGAACAGATCCGCAGAGAGTTACCCCTGCACGACCACCTTCGGGAAGAGGCCAGAGTG 5277

Qy      601 TACTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCC 660
      | ||| |||| | |||| | ||||| ||||| ||||| || || ||||
Db      5278 TGCTGGGTCAGCTCCGCCTGGGCCGCACAGGGGACCGCCCGCACCTTTGTGCGCGTCC 5337

Qy      661 ACGTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTG 720
      ||||| ||||| ||||| || |||| | ||||| ||||| ||||| |
Db      5338 ACGTGCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCG 5397

Qy      721 ACGGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCT 780
      || || | ||||| | |||| | ||||| ||||| || ||||| || ||
Db      5398 ACAGCGCTTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTT 5457

Qy      781 TTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGG 840
      | ||||| ||||| ||||| ||||| | ||||| ||||| ||||| |||||
Db      5458 TCGTGGTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCCAGGGCG 5517

Qy      841 ACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGG 900
      | |||| | ||||| ||||| | |||| | |||| | ||||| |||||
Db      5518 ATGTGACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAGACTTTGCCCTGCTCA 5577

Qy      901 TGCACTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCGCCTACCTGG 960
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5578 CACAGTGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGG 5637

Qy      961 CTGGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGA 1020
      |||| | |||| | |||| | |||| | |||| | |||| | |||| |
Db      5638 CTGGCGGAGACACTGTCTACCTGGCCAACCTTCACCCTGCCAGACTCTGAGTTCTGAAGA 5697

Qy      1021 TCTTTAAACCCGAGGCTGCCTTCCTGCCCAGTGGGTGGGCATTAATGCAGACTTGTCTC 1080
      ||||| || |||| | |||| | |||| | |||| | |||| | |||| |
Db      5698 TCTTTAAGCCGGAGGCGGCCTTCCTGCCCAGTGGGTGGGCATTAATGCAGACTTGTCTC 5757

Qy      1081 CACTCCAGATGTTGGCTGGGCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTC 1140
      |||| | || |||| | |||| | |||| | || || || | || ||
Db      5758 CACTCTGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATC 5815

Qy      1141 AACCCAGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACCTCCGGAGATGCTGGTGG 1200
      | || ||||| || || | || | || || | || || || || || || ||
Db      5816 TTTCTAGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGG 5874

Qy      1201 TCCTGTAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
      | | | || | || | || | ||||| ||||| |||||
Db      5875 TGTTCTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 5921

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RESULT 5
 US-10-105-963-9
 ; Sequence 9, Application US/10105963
 ; Publication No. US20030068818A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Denning, Chris

[illegible]

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Qy      546 CAGATCCGCGAGGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTACTG 605
        |||
Db      641 CAGATCCGCGAGAGTTACCCCTGCACGACCACCTTCGGGAAGAGGCGCAGAGTGTGCTG 700

Qy      606 AGTCAGTTCGGTCTACCCCGCACAGGGGACCGCCCGAGCACCTTCGTGGGGGTCCACGTG 665
        |||
Db      701 GGTACAGTCCGCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTGCGGCTCCACGTG 760

Qy      666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
        |||
Db      761 CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 820

Qy      726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTTGTG 785
        |||
Db      821 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCCGTTCGTG 880

Qy      786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
        |||
Db      881 GTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCGATGTG 940

Qy      846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
        |||
Db      941 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACACAG 1000

Qy      906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCTACCTGGCTGGT 965
        |||
Db     1001 TGCAACCACACCATATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCTACCTGGCTGGC 1060

Qy      966 GGAGATACCATCTACTTGGCTAATTCACCCTGCCCCTTCCAGCTTCCTGAAGATCTTT 1025
        |||
Db     1061 GGAGACACTGTCTACCTGGCCAACTTCACCCTGCCAGACTCTGAGTTCCTGAAGATCTTT 1120

Qy     1026 AAACCCGAGGCTGCCTTCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
        |||
Db     1121 AAGCCGGAGGCGGCCTTCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1180

Qy     1086 CAGATGTTGGCTGGGCCCTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
        |||
Db     1181 TGGACATTGGCTAAGCCTTGA--GAGCCAGGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1238

Qy     1146 AGGGCCAGCGTTATGGGTCGCCGGAAGCCCGAGTAACCTCCGGAGATGCTGGTGGTCTCTG 1205
        |||
Db     1239 AGAGCCAGCAGTACGTGGCTTCAGAGGCCTG-GCATCTTCTGGAGAAGCTTGTGGTGTTC 1297

Qy     1206 TAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
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Db     1298 CTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 1339
    
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RESULT 6

US-11-219-419-9

; Sequence 9, Application US/11219419

; Publication No. US20060057719A1

; GENERAL INFORMATION:

; APPLICANT: Geron Corporation

; APPLICANT: Denning, Chris

; APPLICANT: Clark, A. John

; APPLICANT: Schiff, J. Michael

; TITLE OF INVENTION: CARBOHYDRATE DETERMINANT SELECTION

; FILE REFERENCE: 139/003d


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Qy      606 AGTCAGTTCGGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACGTG 665
        ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      701 GGTACAGTCCGCTGGGCCGCACAGGGGACCGCCCGCGCACCTTTGTGCGCGTCCACGTG 760

Qy      666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      761 CGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGGTGTGGTGGGCGACAGC 820

Qy      726 CGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCGTCTTTGTG 785
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      821 GCCTACCTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTCTTTTCGTG 880

Qy      786 GTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTG 845
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      881 GTCACCAGCAACGGCATGGAGTGGTGTAAGAAAACATCGACACCTCCAGGGCGATGTG 940

Qy      846 ATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAG 905
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      941 ACGTTTGCTGGCGATGGACAGGAGGCTACACCGTGAAAGACTTTGCCCTGCTCACACAG 1000

Qy      906 TGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCTACCTGGCTGGT 965
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1001 TGCAACCACACCATTATGACCATTGGCACCTTCGGCTTCTGGGCTGCCACCTGGCTGGC 1060

Qy      966 GGAGATACCATCTACTTGGCTAACTTACCCTGCCACTTCCAGCTTCCTGAAGATCTTT 1025
        ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1061 GGAGACACTGTCTACCTGGCCAACCTACCCTGCCAGACTCTGAGTTCTGAAGATCTTT 1120

Qy      1026 AAACCCGAGGCTGCCCTTCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1085
        || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1121 AAGCCGGAGGCGGCCCTTCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCACTC 1180

Qy      1086 CAGATGTTGGCTGGGCCCTTGAACCAGCCAGGAGCCTTTCTGGAATAGCCTCGGTCAACCC 1145
        || ||||| ||||| ||||| ||||| || ||||| || ||||| || |||||
Db      1181 TGGACATTGGCTAAGCCTTGA--GAGCCAGGAGACTTTCTGAAGTAGCCTGATCTTTCT 1238

Qy      1146 AGGGCCAGCGTTATGGGTCTCCGGAAGCCCGAGTAACTTCCGGAGATGCTGGTGGTCTTG 1205
        || ||||| || || || || || || || || || || || || || || || || ||
Db      1239 AGAGCCAGCAGTACGTGGCTTCAGAGGCCGTG-GCATCTTCTGGAGAAGCTTGTGGTGTTC 1297

Qy      1206 TAGCAG--GCTGGACACTTATTTCAAGAGTGATTCTAATTGG 1245
        || || ||||| || || ||||| ||||| |||||
Db      1298 CTGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGG 1339
    
```

RESULT 7

US-09-051-034A-1

; Sequence 1, Application US/09051034A

; Patent No. US20010055584A1

; GENERAL INFORMATION:

; APPLICANT: MCKENZIE, IAN FARQUHAR CAMPBELL

; APPLICANT: SANDRIN, MAURO SERGIO

; TITLE OF INVENTION: IMPROVED NUCLEIC ACIDS ENCODING A CHIMERIC

; TITLE OF INVENTION: GLYCOSYLTRANSFERASE

; FILE REFERENCE: 30562.6USWO

; CURRENT APPLICATION NUMBER: US/09/051,034A

; CURRENT FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: PCT/AU97/00492

; PRIOR FILING DATE: 1997-08-01

; PRIOR APPLICATION NUMBER: 60/024,279

; PRIOR FILING DATE: 1996-08-21

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; PRIOR APPLICATION NUMBER: PO1402
; PRIOR FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1043
; TYPE: DNA
; ORGANISM: Sus Domesticus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9)..(1031)
US-09-051-034A-1
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Query Match 35.8%; Score 454.2; DB 3; Length 1043;
 Best Local Similarity 71.8%; Pred. No. 2e-123;
 Matches 610; Conservative 0; Mismatches 233; Indels 6; Gaps 1;

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Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGTTTGGGAACCAGATGGGACAGTATGCCACG 302
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Db      183 GGCATGTGGACGATCAATGCCATCGCCGCCTGGGAACCAGATGGGGGAGTACGCCACC 242

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCC 362
      ||| || |||| | | |||| | | ||||| ||| | |||| |
Db      243 CTGTACGCGCTGGCCAGGATGAACGGGCGGCCGCCCTTCATCCCCGCCGAGATGCACAGC 302

Qy      363 GTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCAC 422
      ||||| || | || | |||| | | |||| | | |
Db      303 ACGCTGGCCCCCATCTTCAGGATCACCTCCCGGTCTCTGCACGCCAGCACGGCCCGCAGG 362

Qy      423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCACCTTAAAG 482
      || |||| | | | || ||||| ||| || |||| |
Db      363 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGCGGTACCGCCACATCCCG 422

Qy      483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
      | | | || | |||| |||| ||||| ||||| ||||| ||
Db      423 GGGGAGTACGTGCGCCTCACGGGTACCCCTGCTCCTGGACCTTCTACCACCACCTGCGC 482

Qy      543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA 602
      |||| | | ||||| |||| |||| | | ||||| ||
Db      483 ACCGAGATCCTCCGGGAGTTCACCCTGCATAACCACGTGCGCGAGGAGGCCAGGATTTC 542

Qy      603 CTGAGTCAGTTCGCTTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
      ||| | |||| | | || |||| | | |||| | ||||| |||
Db      543 CTGCG-----GGGTCTGCGGGTGAACGGGAGCCGACCGAGTACCTACGTGGGGGTGCAC 596

Qy      663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
      ||||| ||||| ||| ||||| ||||| ||||| ||||| |||
Db      597 GTGCGCCGCGGGGACTACGTGCACGTGATGCCCAACGTGTGGAAGGGCGTGGTGGCCGAC 656

Qy      723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCGTCTTT 782
      | | |||| ||||| ||||| ||||| || || | ||||| |||
Db      657 CGGCGGTACCTGGAGCAGGCCCTGGACTGGTTCCGGGCTCGCTACCGCTCCCCCGTCTTT 716

Qy      783 GTGGTCAACAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
      ||||| ||||| ||||| |||| | | |||| | |||| | | ||
Db      717 GTGGTCTCCAGCAACGGCATGGCCTGGTGTGCGGAAAACATCAATGCCTCGCGCGGCGAT 776

Qy      843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGCGCTGCTGGTG 902
      ||| | |||| || |||| |||| | | |||| | |||| | |
Db      777 GTGGTGTTTGCCGGCAATGGCATCGAGGGCTCCCCGCCAAAGACTTCGCGCTGCTCAGC 836
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Qy      903 CAGTGCAACCACACCATCATGACCATTTGGCACCTTCGGCTTCTGGGCCGCTACCTGGCT 962
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      837 CAGTGTAACCACACTGTCATGACCATTTGGCACGTTTCGGGATCTGGGCCGCTACCTTGCT 896

Qy      963 GGTGGAGATACCATCTACTTTGGCTAACTTCACCCTGCCCATTCCAGCTTCCTGAAGATC 1022
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      897 GGTGGAGAGACCATCTACCTGGCCAATTACACGCTCCCGACTCTCCCTTCCTCAAACCTC 956

Qy      1023 TTAAACCCGAGGCTGCCTTCCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      957 TTAAAGCCCGAGGCAGCCTTCCTGCCCCGAGTGGATTGGGATCGAGGCAGACCTGTCCCCA 1016

Qy      1083 CTCCAGATG 1091
        ||||| ||
Db      1017 CTCCTTAAG 1025
    
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RESULT 8

US-09-254-077A-5

; Sequence 5, Application US/09254077A

; Publication No. US20020031494A1

; GENERAL INFORMATION:

; APPLICANT: SANDRIN, MAURO S.

; APPLICANT: MCKENZIE, IAN C. F.

; TITLE OF INVENTION: NUCLEIC ACIDS FOR REDUCING CARBOHYDRATE EPITOPES

; FILE REFERENCE: 30562.5USWO

; CURRENT APPLICATION NUMBER: US/09/254,077A

; CURRENT FILING DATE: 1999-06-11

; PRIOR APPLICATION NUMBER: PCT/AU97/00540

; PRIOR FILING DATE: 1997-08-22

; PRIOR APPLICATION NUMBER: PO 1823

; PRIOR FILING DATE: 1996-08-23

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 1043

; TYPE: DNA

; ORGANISM: Sus scrofa

US-09-254-077A-5

Query Match 35.8%; Score 454.2; DB 3; Length 1043;
 Best Local Similarity 71.8%; Pred. No. 2e-123;
 Matches 610; Conservative 0; Mismatches 233; Indels 6; Gaps 1;

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Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
        ||| ||||| ||| | | ||||| | ||||| ||||| ||||| |||||
Db      183 GGCATGTGGACGATCAATGCCATCGGCCGCTGGGGAACCAGATGGGGGAGTACGCCACC 242

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
        ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| |||||
Db      243 CTGTACGCGCTGGCCAGGATGAACGGCGGCCGGCCTTCATCCCGCCGAGATGCACAGC 302

Qy      363 GTCCTGGCCCCCGTGTTCGCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
        ||||| ||| | ||||| || ||||| || ||||| || |||||
Db      303 ACGCTGGCCCCCATCTTCAGGATCACCTCCCGGTCCTGCACGCCAGCAGGCCCGCAGG 362

Qy      423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
        || |||| | | || || ||||| |||| || ||||| |||
Db      363 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGCGGTACCGCCACATCCCG 422

Qy      483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTCCACCACCTCCGG 542
    
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Db      423  GGGGAGTACGTGCGCCTCACGGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTGCGC  482
Qy      543  GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA  602
      ||||| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      483  ACCGAGATCCTCCGGGAGTTACCCCTGCATAACCACGTGCGCGAGGAGGCCAGGATTTC  542
Qy      603  CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC  662
      ||| | |||| | | ||| ||| ||| ||| ||||| ||||| |||||
Db      543  CTGCG-----GGGTCTGCGGGTGAACGGGAGCCGACCGAGTACCTACGTGGGGGTGCAC  596
Qy      663  GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC  722
      ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      597  GTGCGCCGCGGGGACTACGTGCACGTGATGCCCAACGTGTGGAAGGGCGTGGTGGCCGAC  656
Qy      723  GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTT  782
      | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      657  CGGCGGTACCTGGAGCAGGCCCTGGACTGGTTCCGGGCTCGCTACCGCTCCCCCGTCTTT  716
Qy      783  GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC  842
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      717  GTGGTCTCCAGCAACGGCATGGCCTGGTGTGCGGAAACATCAATGCCTCGCGCGGCGAT  776
Qy      843  GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG  902
      ||| | |||| ||| |||| |||| | | ||||| ||||| ||||| |||||
Db      777  GTGGTGTTTGCCGGAATGGCATCGAGGGCTCCCCCGCCAAAGACTTCGCGCTGCTCACG  836
Qy      903  CAGTGCAACCACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT  962
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      837  CAGTGTAACCACACTGTCATGACCATTGGCACGTTCGGGATCTGGGCCGCCTACCTTGCT  896
Qy      963  GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCAGCTTCTGAAGATC  1022
      ||||| ||||| ||||| ||||| ||| ||| ||| ||| ||| ||||| |||||
Db      897  GGTGGAGAGACCATCTACCTGGCCAATTACACGCTCCCGGACTCTCCCTTCTCAAATC  956
Qy      1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA  1082
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      957  TTTAAGCCCGAGGCAGCCTTCCTGCCCGAGTGGATTGGGATCGAGGCAGACCTGTCCCA  1016
Qy      1083 CTCCAGATG 1091
      |||| | |
Db      1017 CTCCTTAAG 1025

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RESULT 9

US-09-954-456-45

; Sequence 45, Application US/09954456

; Patent No. US20020115057A1

; GENERAL INFORMATION:

; APPLICANT: Young, Paul

; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Ca

; TITLE OF INVENTION: Sets

; FILE REFERENCE: 689290-76

; CURRENT APPLICATION NUMBER: US/09/954,456

; CURRENT FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: US/60/233,617

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US/60/234,052

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: US/60/234,923

; PRIOR FILING DATE: 2000-09-25

; PRIOR APPLICATION NUMBER: US/60/235,134
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,637
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,638
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,711
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,720
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,840
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,863
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 2276
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 45
 ; LENGTH: 3088
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-954-456-45

Query Match 35.4%; Score 449.4; DB 3; Length 3088;
 Best Local Similarity 71.5%; Pred. No. 6.8e-122;
 Matches 607; Conservative 0; Mismatches 236; Indels 6; Gaps 1;

Qy	243	GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG	302
Db	295	GGGATGTGGACGATCAATGCAATAGGCCGCTGGGGAACCAGATGGGCGAGTACGCCACA	354
Qy	303	CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCC	362
Db	355	CTGTACGCCCTGGCCAAGATGAACGGCGGCCCGCCTTCATCCCGGCCAGATGCACAGC	414
Qy	363	GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC	422
Db	415	ACCCTGGCCCCCATCTTCAGAAATCACCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG	474
Qy	423	GTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG	482
Db	475	ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG	534
Qy	483	GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG	542
Db	535	GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC	594
Qy	543	GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA	602
Db	595	CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCAGAAGTTC	654
Qy	603	CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCGACACCTTCGTGGGGGTCCAC	662
Db	655	CTGCG-----GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT	708
Qy	663	GTGCGCCGCGGGGACTATCTGCGTGTGATGCCAAGCGCTGGAAGGGGGTGGTGGGTGAC	722
Db	709	GTTCCGCCGAGGGGACTATGTCCATGTATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC	768
Qy	723	GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTT	782
Db	769	CGGCGATACCTACAGCAGGCCCTGGACTGGTTCGAGCTCGCTACAGCTCCCTCATCTTC	828


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Qy      783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
        ||||| || ||||| ||||| || ||||| ||||| || ||
Db      829 GTGGTCACCAGTAATGGCATGGCCTGGTGTGCGGAGAACATTGACACCTCCCACGGTGAT 888

Qy      843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGCGCTGCTGGTG 902
        ||| | ||||| ||||| ||||| | | ||||| || ||||| || ||
Db      889 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948

Qy      903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
        ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |
Db      949 CAGTGTAACCACACCATCATGACCATTGGGACGTTTCGGGATCTGGGCCGCATACCTCACG 1008

Qy      963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGATC 1022
        || ||||| ||||| ||||| || | ||||| || || ||||| || ||
Db      1009 GCGGAGACACCATCTACCTGGCCAATTACACCTCCCGACTCCCCTTTCCTCAAAATC 1068

Qy      1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
        ||||| || ||||| ||||| ||||| ||||| || ||||| ||||| ||
Db      1069 TTTAAGCCAGAGGCAGCCTTCCTGCCCGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC 1128

Qy      1083 CTCCAGATG 1091
        | | | |
Db      1129 TTAACAAG 1137

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RESULT 10

US-09-954-456-1621

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; Sequence 1621, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Ca
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1621
; LENGTH: 3088

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Db      1069 TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC 1128

Qy      1083 CTCCAGATG 1091
          || |||
Db      1129 TTACTCAAG 1137
    
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RESULT 11

US-09-969-347-234

; Sequence 234, Application US/09969347

; Patent No. US20020115085A1

; GENERAL INFORMATION:

; APPLICANT: Ebner, Reinhard

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa

; TITLE OF INVENTION: Sets

; FILE REFERENCE: 689290-69

; CURRENT APPLICATION NUMBER: US/09/969,347

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US/60/237,598

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: US/60/237,604

; PRIOR FILING DATE: 2000-10-03

; NUMBER OF SEQ ID NOS: 318

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 234

; LENGTH: 3088

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-969-347-234

Query Match 35.4%; Score 449.4; DB 3; Length 3088;
 Best Local Similarity 71.5%; Pred. No. 6.8e-122;
 Matches 607; Conservative 0; Mismatches 236; Indels 6; Gaps 1;

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Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
          |||| ||||| || | | |||| | ||||| ||||| ||||| |||||
Db      295 GGGATGTGGACGATCAATGCAATAGGCCGCCCTGGGAACCAGATGGGCGAGTACGCCACA 354

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCC 362
          ||| ||||| || | |||| | | ||||| || | ||||| || |
Db      355 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCCAGATGCACAGC 414

Qy      363 GTCCTGGCCCCCGTGTTCGCGATCAGCTGCCTGTCTCTGGCGCCCGAGGTAGACAGGCAC 422
          ||||| || | || | |||| | || | || | || | || |
Db      415 ACCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy      423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
          || |||| | | | || ||||| || |||| | |||| |
Db      475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534

Qy      483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
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Db      535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy      543 GAGCAGATCCGCAGCGAGTTCACCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA 602
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Db      595 CAGGAGATCCTCCAGGAGTTCACCTGCACGACCACGTGCGGGAGGAGGCCAGAAAGTTC 654

Qy      603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
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Db      655 CTGCG-----GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708
Qy      663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
      || ||||| ||||| || || ||||| || ||||| ||||| |||||
Db      709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768
Qy      723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCGATACGAAGCCCCCGTCTTT 782
      | || ||||| ||||| ||||| ||||| || || ||||| |||||
Db      769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828
Qy      783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      829 GTGGTCACCAGTAATGGCATGGCCTGGTGTGCGGAGAACATTGACACCTCCCACGGTGAT 888
Qy      843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGCGCTGCTGGTG 902
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Db      889 GTGGTGTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948
Qy      903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
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Db      949 CAGTGTAACCACACCATCATGACCATTGGGACGTTTCGGGATCTGGGCCGCATACCTCAG 1008
Qy      963 GGTGGAGATACCATCTACTTGGCTAACTTCACCTGCCCACTTCCAGCTTCTTGAAGATC 1022
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Db      1009 GCGGAGACACCATCTACCTGGCCAATTACACCTCCCGACTCCCCTTTCTCAAATC 1068
Qy      1023 TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
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Db      1069 TTTAAGCCAGAGGCAGCCTTCCTGCCGAGTGACAGGGATTGCCCGAGACCTGTCCCCC 1128
Qy      1083 CTCCAGATG 1091
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Db      1129 TTACTCAAG 1137
  
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RESULT 12

US-10-843-641A-3072

; Sequence 3072, Application US/10843641A

; Publication No. US20050064454A1

; GENERAL INFORMATION:

; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

; TITLE OF INVENTION: Signature Gene Sets

; FILE REFERENCE: 689290-189

; CURRENT APPLICATION NUMBER: US/10/843,641A

; CURRENT FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: US/09/873,367

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US/09/954,531

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: US/09/954,456

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/962,436

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/962,832

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/964,824

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US/09/967,768

; PRIOR FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/09/968,007

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; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3072
; LENGTH: 3088
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-3072
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Query Match          35.4%; Score 449.4; DB 10; Length 3088;
Best Local Similarity 71.5%; Pred. No. 6.8e-122;
Matches 607; Conservative 0; Mismatches 236; Indels 6; Gaps 1;
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Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
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Db      295 GGGATGTGGACGATCAATGCAATAGGCCGCCCTGGGAACCAGATGGGCGAGTACGCCACA 354

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCC 362
      ||| ||||| || | |||| || | ||||| ||||| ||| ||||| |
Db      355 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCGCCCTTCATCCCGGCCAGATGCACAGC 414

Qy      363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCAC 422
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Db      415 ACCCTGGCCCCCATCTTCAGAATCACCTGCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

Qy      423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
      || |||| | | | || || ||||| |||| || || |||| |
Db      475 ATCCCTTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534

Qy      483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
      | | | | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      535 GGGGAGTACGTCCGCTTACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

Qy      543 GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA 602
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Db      595 CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCAGAAAGTTC 654

Qy      603 CTGAGTCAGTTCCGTCTACCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
      ||| | | || | || | || || || || || || || || || || || ||
Db      655 CTGCG-----GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy      663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
      || ||||| ||||| || | || |||| || | ||||| ||||| ||||| |||||
Db      709 GTTCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy      723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCGCGATACGAAGCCCCGTCTTT 782
      | || |||| ||||| ||||| ||||| ||||| || || || || || || || ||
Db      769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828

Qy      783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
      ||||| || || ||||| |||| || || ||||| ||||| || || || || || ||
Db      829 GTGGTCACCAGTAATGGCATGGCCTGGTGTGCGGAGAACATTGACACCTCCACGGGTGAT 888

Qy      843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
      ||| | ||||| ||||| |||| | | || || || || || || || || || ||
Db      889 GTGGTGTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTGCTCTACTCACA 948
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Qy	243	GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG	302
Db	295	GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA	354
Qy	303	CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC	362
Db	355	CTGTACGCCCTGGCCAAGATGAACGGGCGGCCGCCTTCATCCCGGCCAGATGCACAGC	414
Qy	363	GTCCTGGCCCCGTGTTCCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCAC	422
Db	415	ACCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGTCTGCACAGCGCCACGGCCAGCAGG	474
Qy	423	GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG	482
Db	475	ATCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACGCCACTTCCCG	534
Qy	483	GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTCCACCACCTCCGG	542
Db	535	GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC	594
Qy	543	GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCCCAGGGGGTA	602
Db	595	CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCCCAGAAGTTC	654
Qy	603	CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC	662
Db	655	CTGCG-----GGGCCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT	708
Qy	663	GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC	722
Db	709	GTTCCGCCGAGGGGACTATGTCCATGTATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC	768
Qy	723	GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTT	782
Db	769	CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC	828
Qy	783	GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC	842
Db	829	GTGGTCACCAGTAATGGCATGGCCTGGTGTGCGGAGAACATTGACACCTCCCACGGTGAT	888
Qy	843	GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG	902
Db	889	GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA	948
Qy	903	CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT	962
Db	949	CAGTGTAACCACACCATCATGACCATTGGGACGTTTCGGGATCTGGGCCGCATACCTCACG	1008
Qy	963	GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGATC	1022
Db	1009	GGCGGAGACACCATCTACCTGGCCAATTACACCTCCCCGACTCCCTTTCTCAAAATC	1068
Qy	1023	TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA	1082
Db	1069	TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGACAGGGATTGCCGAGACCTGTCCCCC	1128
Qy	1083	CTCCAGATG	1091
Db	1129	TTACTCAAG	1137

RESULT 14

US-10-843-641A-8363

; Sequence 8363, Application US/10843641A

; Publication No. US20050064454A1

; GENERAL INFORMATION:

; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

; TITLE OF INVENTION: Signature Gene Sets

; FILE REFERENCE: 689290-189

; CURRENT APPLICATION NUMBER: US/10/843,641A

; CURRENT FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: US/09/873,367

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US/09/954,531

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: US/09/954,456

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/962,436

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/962,832

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/964,824

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US/09/967,768

; PRIOR FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/09/968,007

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US/09/969,347

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US/09/969,708

; PRIOR FILING DATE: 2001-10-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 8447

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8363

; LENGTH: 3088

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-843-641A-8363

Query Match 35.4%; Score 449.4; DB 10; Length 3088;
Best Local Similarity 71.5%; Pred. No. 6.8e-122;
Matches 607; Conservative 0; Mismatches 236; Indels 6; Gaps 1;

Qy	243	GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG	302
Db	295	GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGGAACCAGATGGGCGAGTACGCCACA	354
Qy	303	CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCC	362
Db	355	CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCAGATGCACAGC	414
Qy	363	GTCTTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTTGGCGCCCGAGGTAGACAGGCAC	422
Db	415	ACCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG	474
Qy	423	GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG	482
Db	475	ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG	534


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Qy      483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
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Db      535 GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTTACCACCACCTCCGC 594

Qy      543 GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCCAGGGGGTA 602
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      595 CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCAGAAAGTTC 654

Qy      603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC 662
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      655 CTGCG-----GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708

Qy      663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      709 GTTCGCCGAGGGGACTATGTCCATGTATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 768

Qy      723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTT 782
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      769 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 828

Qy      783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
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Db      829 GTGGTCACCAGTAATGGCATGGCCTGGTGTGCGGAGAACATTGACACCTCCCACGGTGAT 888

Qy      843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      889 GTGGTGTGTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 948

Qy      903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCGCCTACCTGGCT 962
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Db      949 CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCGCATACTCACG 1008

Qy      963 GGTGGAGATACCATCTACTTGGCTAACTTACCCCTGCCCCACTTCCAGCTTCTGAAGATC 1022
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Db      1009 GCGGAGACACCATCTACCTGGCCAATTACACCCTCCCCGACTCCCCTTTCTCAAAATC 1068

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RESULT 15

US-10-756-149-275

; Sequence 275, Application US/10756149

; Publication No. US20050181375A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS A

; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

; FILE REFERENCE: file

; CURRENT APPLICATION NUMBER: US/10/756,149

; CURRENT FILING DATE: 2004-01-12

; NUMBER OF SEQ ID NOS: 5818

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 275

; LENGTH: 3088

; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-10-756-149-275

Query Match 35.4%; Score 449.4; DB 10; Length 3088;
 Best Local Similarity 71.5%; Pred. No. 6.8e-122;
 Matches 607; Conservative 0; Mismatches 236; Indels 6; Gaps 1;

Qy	243	GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG	302
Db	295	GGGATGTGGACGATCAATGCAATAGGCCGCTGGGGAACCAGATGGGCGAGTACGCCACA	354
Qy	303	CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCC TTCATCCAGCCTGCCATGCACGCC	362
Db	355	CTGTACGCCCTGGCCAAGATGAACGGCGGCCCGCCTTCATCCCGGCCAGATGCACAGC	414
Qy	363	GTCCTGGCCCCCGTGTTCGCGATCAGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC	422
Db	415	ACCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGTCTGCACAGCGCCACGGCCAGCAGG	474
Qy	423	GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG	482
Db	475	ATCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG	534
Qy	483	GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG	542
Db	535	GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC	594
Qy	543	GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA	602
Db	595	CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCAGAAAGTTC	654
Qy	603	CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC	662
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Qy	663	GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC	722
Db	709	GTTCCGCCGAGGGGACTATGTCCATGTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC	768
Qy	723	GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCGATACGAAGCCCCCGTCTTT	782
Db	769	CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC	828
Qy	783	GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC	842
Db	829	GTGGTCACCAGTAATGGCATGGCTGGTGTGCGGAGAACATTGACACCTCCACGGTGAT	888
Qy	843	GTGATCTTTGCTGGCGATGGGCGGGAGGCCCGCCCGCCAGGGACTTTGCGCTGCTGGTG	902
Db	889	GTGGTGTGTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA	948
Qy	903	CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT	962
Db	949	CAGTGTAACCACACCATCATGACCATTGGGACGTTCCGGATCTGGGCCGCATACCTCACG	1008
Qy	963	GGTGGAGATACCATCTACTTGGCTAACTTCACCCTGCCCACTTCCAGCTTCTGAAGATC	1022
Db	1009	GGCGGAGACACCATCTACCTGGCCAATTACACCCTCCCGACTCCCCTTCTCAAAATC	1068
Qy	1023	TTTAAACCCGAGGCTGCCTTCCTGCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA	1082

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 09844268 and Search Result us-09-844-268-12.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: November 13, 2006, 21:00:21 ; Search time 350 Seconds
(without alignments)
7176.665 Million cell updates/sec

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Scoring table: IDENTITY_NUC
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Searched: 2471159 seqs, 989689746 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	447.8	35.3	1784	8	US-11-266-748A-61104	Sequence 61104, A
c 4	371.2	29.3	1076	8	US-11-266-748A-73885	Sequence 73885, A
5	371.2	29.3	1076	8	US-11-266-748A-126696	Sequence 126696,
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7	101.6	8.0	807	8	US-11-266-748A-369805	Sequence 369805,
c 8	101.6	8.0	807	8	US-11-266-748A-453184	Sequence 453184,
c 9	48.6	3.8	36535	6	US-10-561-201-3	Sequence 3, Appli
c 10	48.6	3.8	36604	6	US-10-561-201-2	Sequence 2, Appli
11	47.4	3.7	6573	9	US-11-218-305-13034	Sequence 13034, A
c 12	47	3.7	36462	6	US-10-561-201-1	Sequence 1, Appli
c 13	46.6	3.7	1158	9	US-11-218-305-24825	Sequence 24825, A
14	46.6	3.7	1196	9	US-11-056-355B-63909	Sequence 63909, A
c 15	45	3.5	1217	9	US-11-218-305-24824	Sequence 24824, A
c 16	45	3.5	3458	9	US-11-218-305-24822	Sequence 24822, A
17	43.8	3.5	1382	9	US-11-218-305-8602	Sequence 8602, Ap
c 18	43.8	3.5	35990	7	US-11-177-646-577	Sequence 577, App
c 19	43.8	3.5	35994	7	US-11-177-646-578	Sequence 578, App
20	43.6	3.4	1527	6	US-10-449-902-7630	Sequence 7630, Ap
21	43	3.4	1799	9	US-11-218-305-9772	Sequence 9772, Ap
22	43	3.4	2281	9	US-11-218-305-5693	Sequence 5693, Ap
23	42.8	3.4	1175	6	US-10-449-902-25325	Sequence 25325, A
24	42.8	3.4	1427	6	US-10-449-902-12258	Sequence 12258, A
25	42.6	3.4	1500	6	US-10-449-902-13184	Sequence 13184, A
26	42.4	3.3	888	9	US-11-218-305-18144	Sequence 18144, A
27	42.4	3.3	1316	6	US-10-449-902-322	Sequence 322, App
28	42.4	3.3	1411	6	US-10-449-902-21269	Sequence 21269, A
29	42.4	3.3	3000	6	US-10-449-902-16305	Sequence 16305, A
30	42.2	3.3	1411	9	US-11-218-305-8608	Sequence 8608, Ap
c 31	42.2	3.3	1619	6	US-10-449-902-9837	Sequence 9837, Ap
32	42.2	3.3	2727	9	US-11-218-305-8606	Sequence 8606, Ap
33	42.2	3.3	2820	6	US-10-449-902-25581	Sequence 25581, A
34	42	3.3	1616	9	US-11-056-355B-14145	Sequence 14145, A
35	42	3.3	1725	6	US-10-449-902-7753	Sequence 7753, Ap
36	41.8	3.3	1328	6	US-10-449-902-9788	Sequence 9788, Ap
37	41.8	3.3	2163	6	US-10-449-902-7754	Sequence 7754, Ap
38	41.8	3.3	4589	9	US-11-218-305-10133	Sequence 10133, A
39	41.6	3.3	1344	6	US-10-953-349-28304	Sequence 28304, A
40	41.6	3.3	1344	9	US-11-056-355B-68758	Sequence 68758, A
41	41.6	3.3	1608	6	US-10-449-902-26162	Sequence 26162, A
42	41.4	3.3	1548	6	US-10-449-902-7534	Sequence 7534, Ap
43	41.4	3.3	1717	9	US-11-218-305-8216	Sequence 8216, Ap
44	41.4	3.3	1926	9	US-11-218-305-4011	Sequence 4011, Ap
45	41.2	3.2	433	8	US-11-266-748A-12462	Sequence 12462, A

ALIGNMENTS

RESULT 1

US-11-266-748A-28779

; Sequence 28779, Application US/11266748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

```
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28779
; LENGTH: 3088
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-28779
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Query Match          35.4%; Score 449.4; DB 8; Length 3088;
Best Local Similarity 71.5%; Pred. No. 3.5e-101;
Matches 607; Conservative 0; Mismatches 236; Indels 6; Gaps 1;
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QY      243 GGGACCTGGACTATTTACCCGGATGGCCGTTTGGGAACCAGATGGGACAGTATGCCACG 302
      ||| ||||| || | | |||| | ||||| ||||| ||| |||||
Db      295 GGGATGTGGACGATCAATGCAATAGGCCGCTGGGGAACCAGATGGGCGAGTACGCCACA 354

QY      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCC 362
      ||| ||||| || | |||| | | ||||| || | ||||| |||
Db      355 CTGTACGCCCTGGCCAAGATGAACGGCGGCCCGCCTTCATCCCGGCCAGATGCACAGC 414

QY      363 GTCCTGGCCCCCGTGTTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
      ||||| || | || | |||| | || | || | || | || |
Db      415 ACCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 474

QY      423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
      || |||| | | | ||||| |||| | || |||| |
Db      475 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG 534

QY      483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
      | | | | | ||||| ||||| ||||| ||||| |||||
Db      535 GGGGAGTACGTCCGCTTACCAGGCTACCCCTGCTCCTGGACCTTCTACCACCACCTCCGC 594

QY      543 GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA 602
      || ||||| | ||||| ||||| |||| | ||||| || |
Db      595 CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCAGAGTTC 654

QY      603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCGAGCACCTTCGTGGGGGTCCAC 662
      ||| | | || | | || | || | |||| | |||||
Db      655 CTGCG-----GGGCTGCAAGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 708
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Qy	663	GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC	722
Db	709	GTTGCGCGAGGGGACTATGTCCATGTATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC	768
Qy	723	GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGGCCGATACGAAGCCCCCGTCTTT	782
Db	769	CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC	828
Qy	783	GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC	842
Db	829	GTGGTCACCAGTAATGGCATGGCCTGGTGTGCGGAGAACATTGACACCTCCACGGTGAT	888
Qy	843	GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG	902
Db	889	GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA	948
Qy	903	CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCCGCTACCTGGCT	962
Db	949	CAGTGTAACCACACCATCATGACCATTGGGACGTTCCGGGATCTGGGCCCGCATACCTCACG	1008
Qy	963	GGTGGAGATACCATCTACTTGGCTAACTTCACCTGCCACTTCCAGCTTCTGAAGATC	1022
Db	1009	GGCGGAGACACCATCTACCTGGCCAATTACACCTCCCCGACTCCCCCTTCTCAAATC	1068
Qy	1023	TTAAACCCGAGGCTGCCTTCCTGCCCCAGTGGGTGGGCATTAATGCAGACTTGTCTCCA	1082
Db	1069	TTAAGCCAGAGGCAGCCTTCCTGCCGAGTGGACAGGGATTGCCGAGACCTGTCCCCC	1128
Qy	1083	CTCCAGATG	1091
Db	1129	TTACTCAAG	1137

RESULT 2

US-11-266-748A-56661

; Sequence 56661, Application US/11266748A

; Publication No. US20060134663A1

GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: US 60/662,276

; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 56661
 ; LENGTH: 3088
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-56661

Query Match 35.4%; Score 449.4; DB 8; Length 3088;
 Best Local Similarity 71.5%; Pred. No. 3.5e-101;
 Matches 607; Conservative 0; Mismatches 236; Indels 6; Gaps 1;

Qy	243	GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG	302
Db	295	GGGATGTGGACGATCAATGCAATAGGCCGCCCTGGGAACCAGATGGGCGAGTACGCCACA	354
Qy	303	CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCATCATCCAGCCTGCCATGCACGCC	362
Db	355	CTGTACGCCCTGGCCAAGATGAACGGCGGCCGCCCTTCATCCCGGCCAGATGCACAGC	414
Qy	363	GTCCTGGCCCCCGTGTTCGCGATCACGCTGCCGTGCTCTGGCGCCCGAGGTAGACAGGCAC	422
Db	415	ACCCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGTCTGCACAGCGCCACGGCCAGCAGG	474
Qy	423	GTCCTTGGCGGGAGCTGGAGCTTACGACTGGATGTCCGAGGATTATGCCCACTTAAAG	482
Db	475	ATCCCTTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACTTCCCG	534
Qy	483	GAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCTGGACCTTCTTCCACCACCTCCGG	542
Db	535	GGGGAGTACGTCCGCTTACCGGCTACCCCTGCTCTGGACCTTCTACCACCACCTCCGC	594
Qy	543	GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA	602
Db	595	CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCAGAAGTTC	654
Qy	603	CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC	662
Db	655	CTGCG-----GGGCCTGCAGGTGAACGGGAGCGCGCGGGCACCTTTGTAGGGGTCCAT	708
Qy	663	GTGCGCCGCGGGGACTATCTGCGTGTGATGCCAAGCGCTGGAAGGGGGTGGTGGGTGAC	722
Db	709	GTTGCGCCGAGGGGACTATGTCCATGTATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC	768
Qy	723	GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTT	782
Db	769	CGGCGATACCTACAGCAGGCCCTGGACTGGTTCGAGCTCGCTACAGCTCCCTCATCTTC	828
Qy	783	GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC	842
Db	829	GTGGTCACCAGTAATGGCATGGCCTGGTGTGCGGAGAACATTGACACCTCCACGGTGAT	888
Qy	843	GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG	902
Db	889	GTGGTGTGTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA	948
Qy	903	CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCGGCCTACCTGGCT	962
Db	949	CAGTGTAACCACACCATCATGACCATTGGGACGTTCGGGATCTGGGCGCATACCTCACG	1008


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Qy      963 GGTGGAGATACCATCTACTTGGCTAACTTCACCCCTGCCCACTTCCAGCTTCCTGAAGATC 1022
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Db      1009 GCGGGAGACACCATCTACCTGGCCAATTACACCCCTCCCGACTCCCCTTTCCTCAAAATC 1068

Qy      1023 TTTAAACCCGAGGCTGCCTTCCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
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Db      1069 TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGGACAGGGATTGCCGCAGACCTGTCCCCC 1128

Qy      1083 CTCCAGATG 1091
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Db      1129 TTAACAAG 1137
  
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RESULT 3

US-11-266-748A-61104

; Sequence 61104, Application US/11266748A

; Publication No. US20060134663A1

; GENERAL INFORMATION:

; APPLICANT: Harkin, Paul

; APPLICANT: Johnston, Patrick

; APPLICANT: Mulligan, Karl

; TITLE OF INVENTION: Transcriptome Microarray Technology and

; TITLE OF INVENTION: Methods of Using the Same

; FILE REFERENCE: 55815-0102 (319189)

; CURRENT APPLICATION NUMBER: US/11/266,748A

; CURRENT FILING DATE: 2005-11-03

; PRIOR APPLICATION NUMBER: EP 04105479.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105483.4

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105507.0

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105485.9

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: EP 04105484.2

; PRIOR FILING DATE: 2004-11-03

; PRIOR APPLICATION NUMBER: US 60/662,276

; PRIOR FILING DATE: 2005-03-14

; PRIOR APPLICATION NUMBER: US 60/700,293

; PRIOR FILING DATE: 2005-07-18

; NUMBER OF SEQ ID NOS: 483996

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 61104

; LENGTH: 1784

; TYPE: DNA

; ORGANISM: Homo Sapiens

US-11-266-748A-61104

Query Match 35.3%; Score 447.8; DB 8; Length 1784;

Best Local Similarity 71.4%; Pred. No. 7.1e-101;

Matches 606; Conservative 0; Mismatches 237; Indels 6; Gaps 1;

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Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
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Db      245 GGGATGTGGACGATCAATGCGATAGGCCGCGCTGGGAACCAGATGGGCGAGTACGCCACA 304

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
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Db      305 CTGTATGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCAGATGCACAGC 364
Qy      363 GTCCTGGCCCCCGTGTCCGCATCACGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC 422
        ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      365 ACCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 424
Qy      423 GCTCCTTGCGGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
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Db      425 ATCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACATCCCG 484
Qy      483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
        || | | | ||| ||| ||| ||| ||| ||| ||| |||
Db      485 GGGGAGTACGTCCGCTTACCAGGCTACCCCTGCTCCTAGACCTTCTACCACCACCTCCGC 544
Qy      543 GAGCAGATCCGCAGCGAGTTCACCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA 602
        || ||| || | ||| ||| ||| ||| ||| ||| |||
Db      545 CAGGAGATCCTCCAGGAGTTCACCCTGCACGACCACGTGCGGGAGGAGGCCAGAAAGTTC 604
Qy      603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCAGCACCTTCGTGGGGGTCCAC 662
        ||| | | || | | || | || | ||| ||| ||| |||
Db      605 CTGCG-----GGGCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT 658
Qy      663 GTGCGCCGCGGGGACTATCTGCGTGTGATGCCAAGCGCTGGAAGGGGGTGGTGGGTGAC 722
        || ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      659 GTTCGCCGAGGGGACTATGTCCATGTATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC 718
Qy      723 GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTT 782
        | || ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      719 CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC 778
Qy      783 GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC 842
        ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      779 GTGGTCACCAGTAATGGCATGGCTGGTGTGCGGAGAACATTGACACCTCCCACAGTGAT 838
Qy      843 GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG 902
        ||| | ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      839 GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA 898
Qy      903 CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT 962
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Db      899 CAGTGTAACCACACCATCATGACCATTGGGACGTTCCGGGATCTGGGCCGCATACCTCACG 958
Qy      963 GGTGGAGATACCATCTACTTGGCTAACTTACCCTGCCCCACTTCCAGCTTCTGAAGATC 1022
        || ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      959 GCGGGAGACACCATCTACCTGGCCAATTACACCTCCCCGACTCCCCTTTCTCAAATC 1018
Qy      1023 TTTAAACCCGAGGCTGCCTTCCTGCCCCGAGTGGGTGGGCATTAATGCAGACTTGTCTCCA 1082
        ||||| || ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1019 TTTAAGCCAGAGGCAGCCTTCCTGCCGGAGTGACGGGGATTGCCGCAGACCTGTCCCCC 1078
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Db      1079 TTAACAAG 1087
    
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RESULT 4
 US-11-266-748A-73885/c
 ; Sequence 73885, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul

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; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73885
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-73885
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Query Match          29.3%; Score 371.2; DB 8; Length 1076;
Best Local Similarity 70.5%; Pred. No. 5.2e-82;
Matches 512; Conservative 0; Mismatches 208; Indels 6; Gaps 1;
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Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
      ||| |||| || | || |||| | ||||| |||| ||||
Db      782 GGGATGTGGACGATCAATGCGATAGGCCGCCCTGGGAACCAGATGGGCGAGTACGCCACA 723

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCCTTCATCCAGCCTGCCATGCACGCC 362
      ||| ||||| || | |||| || | ||||| || | ||||| |
Db      722 CTGTATGCCCTGGCCAAGATGAACGGGCGGCCGCCCTTCATCCCGGCCCAGATGCACAGC 663

Qy      363 GTCCTGGCCCCCGTGTTCCGCATCACGTGCTGCTGCTGGCGCCCGAGGTAGACAGGCAC 422
      ||||| || | || | |||| |||| || || | || |
Db      662 ACCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 603

Qy      423 GCTCCTTGGCGGGAGCTGGAGCTTACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
      || |||| | | | || ||||| |||| || |||| | |
Db      602 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACATCCCG 543

Qy      483 GAGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG 542
      | | | | | ||||| ||||| ||||| ||||| ||||| |||||
Db      542 GGGGAGTACGTCCGCTTACCGGCTACCCCTGCTCCTAGACCTTCTACCACCACCTCCGC 483

Qy      543 GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA 602
      || ||||| | ||||| ||||| ||||| ||||| |||||
Db      482 CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCAGAAAGTTC 423

Qy      603 CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCGAGCACCTTCGTGGGGGTCCAC 662
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<http://es/ScoreAccessWeb/GetItem.action?AppId=09844268&seqId=824815&ItemName=u...> 11/15/06

; ORGANISM: Homo Sapiens
US-11-266-748A-126696

Query Match 29.3%; Score 371.2; DB 8; Length 1076;
Best Local Similarity 70.5%; Pred. No. 5.2e-82;
Matches 512; Conservative 0; Mismatches 208; Indels 6; Gaps 1;

Qy	243	GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG	302
Db	295	GGGATGTGGACGATCAATGCGATAGGCCGCTGGGGAACCAGATGGGCGAGTACGCCACA	354
Qy	303	CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC	362
Db	355	CTGTATGCCCTGGCCAAGATGAACGGGCGGCCGCCCTTCATCCCGGCCAGATGCACAGC	414
Qy	363	GTCCTGGCCCCCGTGTTCGCGCATCAGCTGCCTGTCCTGGCGCCCGAGGTAGACAGGCAC	422
Db	415	ACCCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG	474
Qy	423	GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG	482
Db	475	ATCCCTTGGCAGAACTACCACCTGAACGACTGGATGGAGGAGGAATACCGCCACATCCCG	534
Qy	483	GAGCCCTGGCTGAAGCTCACCGGCTTCCCCTGCTCCTGGACCTTCTTCCACCACCTCCGG	542
Db	535	GGGGAGTACGTCCGCTTCACCGGCTACCCCTGCTCCTAGACCTTCTACCACCACCTCCGC	594
Qy	543	GAGCAGATCCGCAGCGAGTTACCCCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTA	602
Db	595	CAGGAGATCCTCCAGGAGTTACCCCTGCACGACCACGTGCGGGAGGAGGCCAGAAAGTTC	654
Qy	603	CTGAGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCAC	662
Db	655	CTGCGGG-----GCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCAT	708
Qy	663	GTGCGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGAC	722
Db	709	GTTCCGCCGAGGGGACTATGTCCATGTTCATGCCAAAAGTGTGGAAGGGGGTGGTGGCCGAC	768
Qy	723	GGCCGTTACCTCCAGCAGGCTATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTT	782
Db	769	CGGCGATACCTACAGCAGGCCCTGGACTGGTTCCGAGCTCGCTACAGCTCCCTCATCTTC	828
Qy	783	GTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGAC	842
Db	829	GTGGTCACCAGTAATGGCATGGCCTGGTGTGCGGAGAACATTGACACCTCCACAGTGAT	888
Qy	843	GTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTG	902
Db	889	GTGGTGTTTGCTGGCGATGGCATTGAGGGCTCACCTGCCAAAGATTTTGCTCTACTCACA	948
Qy	903	CAGTGCAACCACACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCT	962
Db	949	CAGTGTAACCACACCATCATGACCATTGGGACGTTGGGGATCTGGGCCGCATACCCCTCG	1008
Qy	963	GGTGGG	968
Db	1009	TGTTGA	1014

RESULT 6

```

US-11-266-748A-210852/c
; Sequence 210852, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 210852
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-210852

```

Query Match 16.5%; Score 210; DB 8; Length 1000;
Best Local Similarity 69.1%; Pred. No. 3.7e-42;
Matches 318; Conservative 0; Mismatches 135; Indels 7; Gaps 2;

QY	365	CCTGGCCCCCGTGTTCGCGCAT-CACGCTGCCTTGCTCCGGCCCCAGGTTAGACAGGCCACG	423
Db	454		
QY	424	CTCCTTGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACCTTAAAGG	483
Db	394	TCCCCCTGGCAGAATACTACCACCTGAACGTCTGGATGGAGGAGGAATACCGCCACATCCCGG	335
QY	484	AGCCCTGGCTGAAGCTCACCGGCTTCCCTGCTCCTGGACCTTCTTCCACCACCTCCGGG	543
Db	334		
QY	544	AGCAGATCCGCAGCGAGTTCAACCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTAC	603
Db	274		
QY	604	TGAGTCAGTTCCGCTACCCCGCACAGGGGACCGCCCCAGCACCTTCGTGGGGGTCCACG	663
Db	214		
QY	664	TGCG-----GGGCCTGCAGGTGAACGGGAGCCGGCCGGGCACCTTTGTAGGGGTCCATG	723

RESULT 7

Query Match 8.0%; Score 101.6; DB 8; Length 807;
Best Local Similarity 63.5%; Pred. No. 2.2e-15;
Matches 188; Conservative 0; Mismatches 104; Indels 4; Gaps 2;

```

Qy      363 GTCCTGGCCCCCGTGTTCGCGATCACGCTGCCTGTCTGGCGCCCCGAGGTAGACAGGCAC 422
          ||||| ||| | ||| ||| ||| ||| ||| |||
Db      386 ACCCTGGCCCCCATCTTCAGAATCACCTGCCGGTGTGTGCACAGCGCCACGGCCAGCAGG 445

Qy      423 GCTCCTTGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCACTTAAAG 482
          || ||| | | ||| ||| ||| ||| ||| ||| ||| |||
Db      446 ATCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGGAGAATACCGCCACCTCCCG 505

Qy      483 GAGCCCT--GGCTGAAGCTCACCGGCTT--CCCCTGCTCCTGGACCTTCTTCCACC 534
          | | | | | ||||| | ||| ||||| ||||| |||||
Db      506 GGGGGATTACGTTCCGCTTCACCGGCCTACCCCTGGCTCCTAGACCTTCTACCACC 561
  
```

RESULT 8

```

US-11-266-748A-453184/c
; Sequence 453184, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 453184
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-453184
  
```

```

Query Match      8.0%; Score 101.6; DB 8; Length 807;
Best Local Similarity 63.5%; Pred. No. 2.2e-15;
Matches 188; Conservative 0; Mismatches 104; Indels 4; Gaps 2;
  
```

```

Qy      243 GGGACCTGGACTATTTACCCGGATGGCCGGTTTGGGAACCAGATGGGACAGTATGCCACG 302
          |||| |||| | | | |||| | ||||| ||||| ||| ||||
Db      542 GGGATGTGGACGATCAATGCAATAGGCCGCCTGGGAACCAGATGGGCGAGTACGCCACA 483

Qy      303 CTGCTGGCCCTGGCGCAGCTCAACGGCCGCCAGGCCTTCATCCAGCCTGCCATGCACGCC 362
          ||| ||||| || | |||| || | ||||| || | ||||| |
Db      482 CTGTACGCCCTGGCCAAGATGAACGGGCGGCCCGCCTTCATCCCGGCCAGATGCACAGC 423
  
```



```

Qy      363 GTCCTGGCCCCCGTGTTCGCATCACGCTGCCTGTCTGGCGCCCGAGGTAGACAGGCAC 422
          ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      422 ACCCTGGCCCCCATCTTCAGAAATCACCTGCCGGTGCTGCACAGCGCCACGGCCAGCAGG 363

Qy      423 GCTCCTTGGCGGGAGCTGGAGCTTCACGACTGGATGTCCGAGGATTATGCCCCACTTAAAG 482
          || ||| || | || ||| ||| ||| ||| ||| ||| ||| |||
Db      362 ATCCCCTGGCAGAACTACCACCTGAACGACTGGATGGAGGGAGAATACCGCCACCTCCCG 303

Qy      483 GAGCCCT--GGCTGAAGCTCACCGGCTT--CCCCTGCTCCTGGACCTTCTTCCACC 534
          || | || | ||| ||| ||| ||| ||| ||| ||| |||
Db      302 GGGGGATTACGTTCCGCTTCACCGGCCTACCCCTGGCTCCTAGACCTTCTACCACC 247
  
```

RESULT 9

US-10-561-201-3/c

; Sequence 3, Application US/10561201

; Publication No. US20060211115A1

; GENERAL INFORMATION:

; APPLICANT: The Trustees of the University of Pennsylvania

; APPLICANT: Roy, Soumitra

; APPLICANT: Wilson, James M.

; TITLE OF INVENTION: Methods of Generating Chimeric Adenoviruses and Uses For Such

; TITLE OF INVENTION: Chimeric Adenoviruses

; FILE REFERENCE: UPN-P3067PCT

; CURRENT APPLICATION NUMBER: US/10/561,201

; CURRENT FILING DATE: 2005-12-19

; PRIOR APPLICATION NUMBER: US 10/465,302

; PRIOR FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: US 60/566,212

; PRIOR FILING DATE: 2004-04-28

; PRIOR APPLICATION NUMBER: US 60/575,429

; PRIOR FILING DATE: 2004-05-28

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 36535

; TYPE: DNA

; ORGANISM: chimpanzee adenovirus serotype Pan7

US-10-561-201-3

```

Query Match          3.8%; Score 48.6; DB 6; Length 36535;
Best Local Similarity 54.1%; Pred. No. 0.11;
Matches 99; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
  
```

```

Qy      773 CCCCCTCTTTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTC 832
          || | ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7852 CACCTACGATGTGGAACCTACACCTGGATGGGGTCCTTCGGCAAGCAGCTCGTCCCTT 7793

Qy      833 CCGGGGGGACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGC 892
          | | ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7792 CATGCTGGTCATGAACTCTCCGGGGACCCGCCGCTCGTCGAGCTCGCCCACGACCTCGC 7733

Qy      893 GCTGCTGGTGCAGTGCAACCACCATCATGACCATTGGCACCTTCGGCTTCTGGGCCGC 952
          || ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      7732 CCTCCAGCTCAAGTGGGACCGCTGGCACGGCGACCCCGCACCTTCTACTGCGTCACCCC 7673

Qy      953 CTA 955
          ||
Db      7672 CGA 7670
  
```

RESULT 10

US-10-561-201-2/c

```
; Sequence 2, Application US/10561201
; Publication No. US20060211115A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Roy, Soumitra
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Methods of Generating Chimeric Adenoviruses and Uses For Such
; TITLE OF INVENTION: Chimeric Adenoviruses
; FILE REFERENCE: UPN-P3067PCT
; CURRENT APPLICATION NUMBER: US/10/561,201
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: US 10/465,302
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/566,212
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US 60/575,429
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 36604
; TYPE: DNA
; ORGANISM: chimpanzee adenovirus serotype Pan6
US-10-561-201-2
```

```
Query Match          3.8%; Score 48.6; DB 6; Length 36604;
Best Local Similarity 54.1%; Pred. No. 0.11;
Matches 99; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
```

```
Qy      773 C C C C G T C T T T G T G G T C A C C A G C A A C G G C A T G G A G T G G T G C C G G A A G A A C A T C G A C A C C T C 832
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      7846 C A C C T A C G A T G T G G A A C C T A C A C C T G G A T G G G G T C C T T C G G C A A G C A G C T C G T C C C C T T 7787

Qy      833 C C G G G G G G A C G T G A T C T T T G C T G G C G A T G G G C G G G A G G C C G C G C C C G C C A G G G A C T T T G C 892
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      7786 C A T G C T G G T C A T G A A A C T C T C C G G G G A C C G C C G C T C G T C G A G C T C G C C C A C G A C C T C G C 7727

Qy      893 G C T G C T G G T G C A G T G C A A C C A C A C C A T C A T G A C C A T T G G C A C C T T C G G C T T C T G G G C C G C 952
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      7726 C C T C C A G C T C A A G T G G G A C C G C T G G C A C G G C G A C C C C G C A C C T T C T A C T G C G T C A C C C C 7667

Qy      953 C T A 955
      | |
Db      7666 C G A 7664
```

RESULT 11

US-11-218-305-13034

```
; Sequence 13034, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
```

```
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13034
; LENGTH: 6573
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (214)..(214)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1342)..(1342)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3788)..(3788)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5035)..(5035)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5217)..(5217)
; OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-13034
```

Query Match 3.7%; Score 47.4; DB 9; Length 6573;
 Best Local Similarity 48.0%; Pred. No. 0.12;
 Matches 135; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

```
Qy      683 GCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGCCGTTACCTCCAGCAGGC 742
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2582 GTGTGTGGGTGTGGGGGGGCGGGGTGGGGTGGGGAGTGACACCCGGGGGCCGATGACGAC 2641

Qy      743 TATGGACTGGTTCCGGGCCCCGATACGAAGCCCCCGTCTTTGTGGTCACCAGCAACGGCAT 802
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2642 GCTGCACATGGACCCGCCGGCGCCGCCGCCGCGCGCCGCTCAGTGTGACAGCTGCGACCT 2701

Qy      803 GGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGACGTGATCTTTGCTGGCGATGG 862
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2702 GCACCCGGGCGAGACGTTACCGGCTTCTGCGCCGCGTGCCTGCGCGAGCGCCTCCACGG 2761

Qy      863 GCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGTGCAAGTCAACACACCATCAT 922
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2762 TCTCGAGGCGTCCGCCCGCCGCCCTCCGCGCCGGGGCGCAAGTCCACATCGGCCATCCG 2821

Qy      923 GACCATTGGCACCTTCGGCTTCTGGGCCGCCTACCTGGCTG 963
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2822 GTCCCTGTTCGCCAGGCCGTTCCGCCCGCGCAGCTCGTCTG 2862
```

RESULT 12
 US-10-561-201-1/c
 ; Sequence 1, Application US/10561201
 ; Publication No. US20060211115A1

```
; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Roy, Soumitra
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Methods of Generating Chimeric Adenoviruses and Uses For Such
; TITLE OF INVENTION: Chimeric Adenoviruses
; FILE REFERENCE: UPN-P3067PCT
; CURRENT APPLICATION NUMBER: US/10/561,201
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: US 10/465,302
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 60/566,212
; PRIOR FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US 60/575,429
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 36462
; TYPE: DNA
; ORGANISM: chimpanzee adenovirus serotype Pan5
US-10-561-201-1
```

```
Query Match          3.7%; Score 47; DB 6; Length 36462;
Best Local Similarity 53.6%; Pred. No. 0.27;
Matches 98; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
```

```
Qy      773 CCCCCTCTTTGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTC 832
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      7840 CACCTACGACGTGGAAACCTACACCTGGATGGGGTCCTTCGGCAAGCAGCTCGTCCCTT 7781

Qy      833 CCGGGGGGACGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCGCCAGGGACTTTGC 892
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      7780 CATGCTGGTCATGAAACTCTCCGGGGACCCGCCGCTCGTCGAGCTCGCCCCACGACCTCGC 7721

Qy      893 GCTGCTGGTGCAAGTGAACACACCATCATGACCATTTGGCACCTTCGGCTTCTGGGCCGC 952
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      7720 CCTCCAGCTCAAGTGGGACCGCTGGCACGGCGACCCCGCACCTTCTACTGCGTCACCCC 7661

Qy      953 CTA 955
      | |
Db      7660 CGA 7658
```

RESULT 13

```
US-11-218-305-24825/c
; Sequence 24825, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24825
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36)..(36)
; OTHER INFORMATION: n is a, c, g, or t
US-11-218-305-24825
```

Query Match 3.7%; Score 46.6; DB 9; Length 1158;
 Best Local Similarity 48.3%; Pred. No. 0.099;
 Matches 130; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

```
QY      272 GTTTGGGAACCAAGATGGGACAGTATGCCACGCTGCTGGCCCTGGCGCAGCTCAACGGCCG 331
      ||| ||| | | | | | | | | | | | | | | | | |
Db      564 GTTCGGGCTCATGTACGCCTACTTTGCGACGGTGATGGACAAAGCGCGGAGGGTCCGCGC 505

QY      332 CCAGGCCCTTCATCCAGCCTGCCATGCACGCCGTCCTGGCCCCCGTGTTCCGCATCACGCT 391
      | ||| | | | | | | | | | | | | | | | | |
Db      504 CGGCGCCGGAGCGCTGGCGGCGCCGCTCGCCGTGGGGCTCCTGGCGGGGGCCAACGTGCT 445

QY      392 GCCTGTCTTGGCGCCCGAGGTAGACAGGCACGCTCCTTGGCGGGAGCTGGAGCTTCACGA 451
      | | | | | | | | | | | | | | | | | | |
Db      444 GGCCTGCGGCGCGCTGGAGGGCGCCGTGATGAATCCGGCGCGCGCTTCGGGCCCCGCCGT 385

QY      452 CTGGATGTCCGAGGATTATGCCCACTTAAAGGAGCCCTGGCTGAAGCTCACCGGCTTCCC 511
      | | | | | | | | | | | | | | | | | | |
Db      384 CGTGGGCTCCCCTCGCTGGAGACCAATGGGTGTACTGGGTGGGGCCCATGGTCGGGCGC 325

QY      512 CTGCTCCTGGACCTTCTTCCACCACCTCC 540
      | | | | | | | | | | | | | | |
Db      324 CGGCCTCTCCGGCGTCGTCTACGAGCACC 296
```

RESULT 14

US-11-056-355B-63909

```
; Sequence 63909, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 63909
; LENGTH: 1196
```

```
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1196)
; OTHER INFORMATION: Ceres Seq. ID no. 12616895
US-11-056-355B-63909
```

```
Query Match          3.7%; Score 46.6; DB 9; Length 1196;
Best Local Similarity 47.4%; Pred. No. 0.1;
Matches 174; Conservative 0; Mismatches 189; Indels 4; Gaps 1;
```

```
Qy      546 CAGATCCGCGAGGAGTTCACCTGCACGACCACCTTCGGCAAGAGGCCAGGGGGTACTG 605
      || ||| || | || ||| | | || || | |||| || | | || |
Db      609 CATGTCTCCGATCTCTCCCCATCCAGTCCGGCTGCTGCAAGCCTCCGATCAGCTGCGG 668

Qy      606 AGTCAGTTCCGTCTACCCCGCACAGGGGACCGCCCGAGCACCTTCGTGGGGGTCCACGTG 665
      ||| | |||| || | | || ||||| || | || || | || ||
Db      669 CTTACCTACGTCAACAGCACGCAATGGACCGGCCCGCCAAGTCGACGGAGCCCGACTG 728

Qy      666 CGCCGCGGGGACTATCTGCGTGTGATGCCCAAGCGCTGGAAGGGGGTGGTGGGTGACGGC 725
      || |||| || | | || | | || | | || | || || || |
Db      729 CGGCGCGTGGTCCAACGACGGGGCGCTCTGCTACGGCTGCCAGTCGTGCAAGGCCGGCGT 788

Qy      726 CGTTACCTCCAGCAGGC----TATGGACTGGTTCGGGGCCCGATACGAAGCCCCCGTCTT 781
      || || || || || | | | | | | | | || || || || ||
Db      789 GGTGGCCACCCCTCAAGCGCAATTGGAAGCGCTCCGCCATCATCAACATCGTCTTCTCTCGT 848

Qy      782 TGTGGTCACCAGCAACGGCATGGAGTGGTGCCGGAAGAACATCGACACCTCCCGGGGGGA 841
      | ||| || | | | | | ||| | || ||| ||| | || |
Db      849 CTTATCATCATTTGTCTACTCCGTCGGCTGCTGCGCCTTCAGGAACAACCGCCGCGACCA 908

Qy      842 CGTGATCTTTGCTGGCGATGGGCGGGAGGCCGCGCCCGCCAGGGACTTTGCGCTGCTGGT 901
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Db      909 CCGCAACGGCGGGCGGGTACAAGCAGCAGGGCGCGTACGCCTGATCGTTTGGCTCGGTTAT 968

Qy      902 GCAGTGC 908
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Db      969 TTATTGC 975
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RESULT 15

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US-11-218-305-24824/c
; Sequence 24824, Application US/11218305
; Publication No. US20060141495A1
; GENERAL INFORMATION:
; APPLICANT: MONSANTO TECHNOLOGY, LLC
; APPLICANT: McLaird, Paul L.
; APPLICANT: Tao, Nengbing
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
; TITLE OF INVENTION: Corn.
; FILE REFERENCE: 38-21 (53660)B
; CURRENT APPLICATION NUMBER: US/11/218,305
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US 60/606,880
; PRIOR FILING DATE: 2004-09-01
; NUMBER OF SEQ ID NOS: 25043
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24824
; LENGTH: 1217
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; TYPE: DNA
; ORGANISM: Zea mays
US-11-218-305-24824

Query Match 3.5%; Score 45; DB 9; Length 1217;
Best Local Similarity 48.0%; Pred. No. 0.25;
Matches 129; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

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Qy      272 GTTTGGGAACCAGATGGGACAGTATGCCACGCTGCTGGCCCTGGCGCAGCTCAACGGCCG 331
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Db      599 GTTCGGGCTCATGTACGCCTACTTTGCGACGGTGATGGACAAAGCGCGGAGGGTCCGCGC 540

Qy      332 CCAGGCCTTCATCCAGCCTGCCATGCACGCCGTCCTGGCCCCCGTGTCCGCATCACGCT 391
      | ||| | | | | | | | | | | | | | | | |
Db      539 CGGCGCCGGAGCGCTGGCGGCGCCGCTCGCCGTGGGGCTTCTGGCGGGGGCCAACGTGCT 480

Qy      392 GCCTGTCTTGGCGCCCGAGGTAGACAGGCACGCTCCTTGGCGGGAGCTGGAGCTTCACGA 451
      | | | | ||| ||| | | | | | | | | | | |
Db      479 GGCCTGCGGCGCGCTGGAGGGCGCCGTGATGAATCCGGCGCGCGCTTCGGGCCCCGCCGT 420

Qy      452 CTGGATGTCCGAGGATTATGCCCCTTAAAGGAGCCCTGGCTGAAGCTCACCGGCTTCCC 511
      | | ||| | | | | | | | | | | | | | |
Db      419 CGTGGGCTCCCGTCGCTGGAGACACCAATGGGTGTACTGGGTGGGGCCCATGGTCGGCGC 360

Qy      512 CTGCTCCTGGACCTTCTTCCACCACCTCC 540
      | || || | || || || | | |
Db      359 CGGCCTCTCCGGCGTCGTCTACGAGCACC 331
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Search completed: November 14, 2006, 02:47:14
Job time : 353 secs

SCORE 1.3 BuildDate: 12/06/2005